

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 30, 2003, 15:03:47 ; Search time 38 Seconds

(without alignments)

1451.730 Million cell updates/sec

Title: US-09-990-087-17

Perfect score: 211%

Sequence: 1 MGHHHHHIEGRLLKLDND.....SFKVSFSLAEYTKKLNTQ 414

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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3:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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19:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1024	48.3	243	9 AAP81082	Sequence of mature
2	1024	48.3	267	7 AAP61079	Assumed human apol
3	1024	48.3	267	9 AAP82128	Entire human prepr
4	1024	48.3	267	14 AAR34032	Sequence of apo AI
5	1024	48.3	267	16 AAR72705	Human apo A-I incl
6	1024	48.3	267	20 AAY18675	Human apolipoprote
7	1024	48.3	267	22 AAB47620	Full length Apo-AI
8	1024	48.3	267	9 AAP80668	Recombinant human
9	1016	48.0	267	18 AAW08602	Human apolipoprote
10	1014	47.9	264	15 AAR56863	Apo-lipoprotein AI

11	1014	47.9	264	15	AAR56864	Apo-lipoprotein AI
12	990	46.7	299	22	AAU33170	Novel human secret
13	974	46.0	244	22	AAU28184	Novel human secret
14	788	37.2	221	22	AAU29835	Novel human secret
15	726.5	34.3	318	22	AAU30268	Novel human secret
16	643	30.4	359	22	AAU30470	Novel human secret
17	635	30.0	151	22	AAU02278	Human polypeptide
18	541	25.5	119	22	AAU03468	Novel human secret
19	526	24.8	166	22	AAU28372	Novel human secret
20	355	16.8	120	22	AAU30267	Novel human secret
21	355	16.8	120	22	AAU30469	Novel human secret
22	349.5	16.5	373	14	AAR39486	Human apoAIV mutei
23	339	16.0	337	14	AAR39485	Human apoAIV mutei
24	335	15.8	342	14	AAR39487	Human apoAIV mutei
25	324.5	15.3	396	22	AAB90664	Human secreted pro
26	323.5	15.3	363	14	AAR39479	Human apoAIV mutei
27	323.5	15.3	377	14	AAR39443	Human apolipoprote
28	323.5	15.3	377	14	AAR39502	Human apoAIV mutei
29	323.5	15.3	377	14	AAR39501	Human apoAIV mutei
30	321.5	15.2	396	23	AAU10863	Human apolipoprote
31	320.5	15.1	377	14	AAR39499	Human apoAIV mutei
32	320.5	15.1	377	14	AAR39500	Human apoAIV mutei
33	320.5	15.1	396	23	AAU10860	Human apolipoprote
34	320.5	15.1	396	23	AAU10861	Human apolipoprote
35	320.5	15.1	396	23	AAU10865	Human apolipoprote
36	320.5	15.1	396	23	AAU10867	Human apolipoprote
37	320.5	15.1	396	23	AAU10868	Human apolipoprote
38	320.5	15.1	396	23	AAU10869	Human apolipoprote
39	319.5	15.1	363	14	AAR39478	Human apoAIV mutei
40	319.5	15.1	377	14	AAR39480	Human apoAIV mutei
41	319.5	15.1	377	14	AAAR45244	Human apoAIV mutei
42	319.5	15.1	396	23	AAU10864	Human apolipoprote
43	318.5	15.0	377	14	AAAR45243	Human apolipoprote
44	318.5	15.0	396	23	AAU10866	Human apolipoprote
45	317.5	15.0	333	14	AAR39481	Human apoAIV mutei

#### ALIGNMENTS

RESULT 1  
AAP81082  
ID AAP81082 standard; protein; 243 AA.  
XX  
AC AAP81082;  
XX  
DT 14-JAN-1991 (first entry)  
XX  
DE Sequence of mature human apolipoprotein AI (apoAI).  
XX  
KW Atherosclerosis; therapy; cardiovascular disease.  
XX  
OS Homo sapiens.  
XX  
PN WO8803166-A.  
XX  
PD 05-MAY-1988.  
XX  
PF 21-OCT-1987; 87WO-EP00621.  
XX  
PR 23-OCT-1986; 86GB-0025435.  
XX  
(FARM ) FARMITALIA C ERBA SPA.  
XX  
PI Lorenzetti R, Monaco L, Soria M, Palomba R, Isacchi A, Sarmientos P;  
XX  
DR WPI; 1988-133240/19.  
XX  
PT N-PSDB; AAN80243.  
XX  
PT Recombinant human apo-lipoprotein AI -  
XX used to lower plasma cholesterol and/or tri glyceride levels and  
XX to combat atherosclerosis and cardiovascular diseases

PS Disclosure; Fig 1; 5lpp; English.

XX The protein comprising apo AI genetic variants may be used to lower  
 CC plasma cholesterol and/or triglyceride levels. They may also be used to  
 CC combat atherosclerosis and cardiovascular diseases such as coronary  
 CC heart disease. Pred. proteins are Met-apo AI, Met-apo AI-r6, Met-apo  
 CC AI-MI and Met-apo AI-r6/MI.

XX Sequence 243 AA;

Query Match 48.3%; Score 1024; DB 9; Length 243;

Best Local Similarity 88.5%; Pred. No. 2.2e-60;

Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 180 LEDRQGLLPVLESFKVSVFLSALEETTKLNTQGTCLKLDNWDVSTSTFSKLREQLGPVT 239

DB 11 VKDLATVYVDVILKSGRDYVSQFE--GSALGKQLNLKLDNWDVSTSTFSKLREQLGPVT 68

QY 240 QEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQE 299

DB 69 QEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQE 128

QY 300 GARQKLHELQEKLSPLGEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGAR 359

DB 129 GARQKLHELQEKLSPLGEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGAR 188

QY 360 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKVSVFLSALEETTKLNTQ 414

DB 189 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKVSVFLSALEETTKLNTQ 243

#### RESULT 2

AAP61079

ID AAP61079 standard; Protein; 267 AA.

XX AAP61079;

DT 07-OCT-1991 (first entry)

XX Assumed human apolipoprotein A-1 derivative gene product.

DE Hyperlipaemia; arteriosclerosis.

KW Homo sapiens.

OS JP61096998-A.

PN 15-MAY-1986.

PD 16-OCT-1984; 84JP-0216988.

PF 16-OCT-1984; 84JP-0216988.

PT (MITU ) MITSUBISHI CHEM IND KK.

XX WPI; 1986-165025/26.

XX N-PSDB; AAN60886.

XX Human apo.lipoprotein A-1 (deriv.) prepn. - by providing DNA

PT fragment in cloning site downstream of expression vector promoter

PT and introducing into host microorganism.

XX Disclosure; Fig 2; 9pp; Japanese.

PS The human apolipoprotein may be produced by a suitable transformed

CC host, it is effective in treating hyperlipaemia and arteriosclerosis.

XX Sequence 267 AA;

Query Match 48.3%; Score 1024; DB 7; Length 267;

Best Local Similarity 88.5%; Pred. No. 2.5e-60;

Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 180 LEDRQGLLPVLESFKVSVFLSALEETTKLNTQGTCLKLDNWDVSTSTFSKLREQLGPVT 239

DB 35 VKDLATVYVDVILKSGRDYVSQFE--GSALGKQLNLKLDNWDVSTSTFSKLREQLGPVT 92

QY 240 QEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQE 299

DB 93 QEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQE 152

QY 300 GARQKLHELQEKLSPLGEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGAR 359

DB 153 GARQKLHELQEKLSPLGEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGAR 212

QY 360 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKVSVFLSALEETTKLNTQ 414

DB 213 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKVSVFLSALEETTKLNTQ 267

#### RESULT 3

AAP82128

ID AAP82128 standard; protein; 267 AA.

XX AAP82128;

DT 24-OCT-1990 (first entry)

XX Entire human preproapoprotein A1.

DE human preproapoprotein A1; high density lipoprotein deficiency; ss.

KW synthetic.

OS

XX

XX Key

XX Location/Qualifiers

FT Peptide

FT 1..18

FT /label=precursor

FT 19..24

FT /label=propeptide

FT 25..267

FT /label=mature apoprotein

XX EP293357-A.

XX 30-NOV-1988.

XX 24-MAY-1988; 88EP-0870095.

XX 28-MAY-1987; 87GB-0012540.

XX (UNIO ) UCB SA.

XX Bollen A, Gobert J, Wulfert E;

XX WPI; 1988-339891/48.

XX N-PSDB; AAN82064.

XX New DNA encoding human preproapoprotein A1 -

PT modified to eliminate hairpin structures

XX Disclosure; ; p; French.

XX The cDNA 878bp fragment encoding preproapoprotein A1 was detected

CC in clone pULB1609 derived from human liver cells.

CC See also AAN81258.

XX Sequence 267 AA;

Query Match 48.3%; Score 1024; DB 9; Length 267;

Best Local Similarity 88.5%; Pred. No. 2.5e-60;

Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 180 LEDRQGLLPVLESFKVSVFLSALEETTKLNTQGTCLKLDNWDVSTSTFSKLREQLGPVT 239

DB 35 VKDLATVYVDVILKSGRDYVSQFE--GSALGKQLNLKLDNWDVSTSTFSKLREQLGPVT 92

QY 240 QEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDQFQKKWQEMELYRQKVEPLRAELQ 299  
 DB 93 QEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDQFQKKWQEMELYRQKVEPLRAELQ 152  
 QY 300 GARQKLHELQKLSPLGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 359  
 DB 153 GARQKLHELQKLSPLGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 212  
 QY 360 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESEKVSFSLSALEEYTKKLNTQ 414  
 DB 213 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESEKVSFSLSALEEYTKKLNTQ 267

RESULT 4  
 AAR34032  
 ID AAR34032 standard; Protein; 267 AA.  
 XX  
 AC AAR34032;  
 XX  
 DT 13-AUG-1993 (first entry)  
 XX  
 DE Sequence of apo AI.  
 XX  
 KW Lipoprotein; apoprotein; B-100; A-I; LDL; HDL; assay.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09307165-A.  
 XX  
 PD 15-APR-1993.  
 XX  
 PF 09-OCT-1992; 92WO-US08634.  
 XX  
 PR 09-OCT-1991; 91US-0774633.  
 PR 08-OCT-1992; 92US-0555555.  
 PR 28-JUN-1992; 92US-0901706.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Curtiss LK, Koduri KR, Smith RS, Witztum JL, Young SG;  
 XX  
 DR WPI; 1993-134378/16.  
 DR N-PSDB; AAQ40030.  
 XX  
 PT Polypeptide mimic of native apo B-100 and native apo A-I - useful  
 in assays for LDL and HDL in plasma samples  
 XX  
 PS Claim 19; Pages 105-106; 137pp; English.  
 XX  
 CC The inventors claim a portion of the polypeptide contg. apo B-100  
 that immunoreacts with antibodies secreted by the hybridoma MB47  
 having ATCC Accession No. 8746. Polypeptides specifically claimed  
 CC include residues 217-297, 216-310, 216-331, 216-352, 216-377, 1-377,  
 CC 205-297, 173-297, 140-297. DNA sequences encoding the polypeptides  
 CC are also claimed. Also claimed are a fusion polypeptide that  
 CC contains: (a) a first amino acid residue sequence up to 250 residues  
 CC in length that includes residues 120-135 of apo A-I. (b) a second  
 CC amino acid residue sequence up to 375 residues in length that  
 CC includes residues 217-297 of apo B-100 and DNA encoding it.  
 XX  
 SQ Sequence 267 AA;

Query Match 48.3%; Score 1024; DB 14; Length 267;  
 Best Local Similarity 88.5%; Pred. No. 2.5e-60;  
 Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 180 LEDLRQGLLPVLESEKVSFSLSALEEYTKKLNTQGLTKLLDNWDSVTFSKLRQLGPVT 239  
 DB 35 VADLATVYVDVLKDSGRDVSQFE--GSAKGKQLNKLKLLDNWDSVTFSKLRQLGPVT 92  
 QY 240 QEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDQFQKKWQEMELYRQKVEPLRAELQ 299  
 DB 93 QEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDQFQKKWQEMELYRQKVEPLRAELQ 152

QY 300 GARQKLHELQKLSPLGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 359  
 DB 153 GARQKLHELQKLSPLGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 212  
 QY 360 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESEKVSFSLSALEEYTKKLNTQ 414  
 DB 213 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESEKVSFSLSALEEYTKKLNTQ 267

RESULT 5  
 AAR72705  
 ID AAR72705 standard; Protein; 267 AA.  
 XX  
 AC AAR72705;  
 XX  
 DT 31-OCT-1995 (first entry)  
 XX  
 DE Human apo A-I including signal and propeptide sequences.  
 XX  
 KW Apo A-I; LDL cholesterol; low density lipoprotein; lipid.  
 XX  
 OS Homo sapiens.  
 XX

Key Location/Qualifiers  
 FT Peptide 1..18  
 FT /label= presignal  
 FT Peptide 19..24  
 FT /label= propeptide  
 FT Peptide 120..135  
 FT /label= claimed  
 FT /note= "as part of fusion polypeptide"  
 FT Peptide 19..240  
 FT /label= claimed  
 FT /note= "as part of fusion polypeptide"

PN US5408038-A.  
 XX  
 XX 18-APR-1995.  
 XX  
 PF 09-OCT-1991; 91US-0774633.  
 XX  
 PR 09-OCT-1991; 91US-0774633.  
 PR 18-JUN-1992; 92US-0501706.  
 PR 08-OCT-1992; 92US-0959946.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Curtiss LK, Koduri KR, Smith RS, Witztum JL, Young SG;  
 XX  
 DR WPI; 1995-161146/21.  
 DR N-PSDB; AAQ89634.  
 XX  
 PT New apo:lipoprotein B-100 peptide(s) and fusion peptide(s) - used  
 in assay systems for detecting LDL and HDL cholesterol levels in  
 PT body fluids.  
 XX  
 PS Claim 10; Fig 2; 4lpp; English.  
 XX  
 CC AAA89634 and AAR72705 depict the AA sequence of human apo A-I and its  
 corresp. cDNA, including presignal residues and propeptide  
 CC residues, according to Seilhamer et al., DNA 3(4):309 (1984).  
 CC A dispersible apo A-I/B-100 fusion polypeptide is claimed which  
 CC contains a first AA sequence of apo A-I and that includes at  
 CC least AA sequence positions 120-135 (see AAR72606) and which reacts  
 CC with pan anti-apo AI antibodies such as: AI-4 ATCC HB8744; AI-7  
 CC ATCC HB 8745; AI-9 ATCC HB 8741; AI-10 ATCC HB 9200; AI-11 ATCC  
 CC HB 9201; AI-12 ATCC HB 9202; AI-13 ATCC HB 9203; AI-14 ATCC HB  
 CC 9204; AI-18 ATCC HB 9507.  
 XX  
 SQ Sequence 267 AA;

Query Match 48.3%; Score 1024; DB 16; Length 267;

Best Local Similarity 88.5%; Pred. No. 2.5e-60;  
Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 180 LEDLRQGLLPVLSFKVSLSALEEYTKKLTQGTGLKLDNDWDSVTSTFSKLRQGLGPTV 239  
Db 35 VKDLATVYVDLVKDSGRDYSQFE--GSALGKQLNLKLDNDWDSVTSTFSKLRQGLGPTV 92  
QY 240 QEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQ 299  
Db 93 QEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQ 152  
QY 300 GARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 359  
Db 153 GARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 212  
QY 360 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLSFKVSLSALEEYTKKLTQ 414  
Db 213 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLSFKVSLSALEEYTKKLTQ 267

## RESULT 6

AA418675  
ID AAY18675 standard; Protein; 267 AA.

XX AC AAY18675;

XX XX 09-JUL-1999 (first entry)

XX DE Human apolipoprotein AI protein sequence.

XX KW Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder;  
KW ApoA-I; cardiovascular disease; atherosclerosis; restenosis; ICAT;  
KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.

XX OS Homo sapiens.

XX XX W09916409-A2.

XX XX 08-APR-1999.

XX XX 28-SEP-1998; 98WO-US20329.

XX XX 29-SEP-1997; 97US-0940136.

XX PA (BUTT/) BUTTNER K.

XX PA (CORN/) CORNUT I.

XX PA (DASS/) DASSEUX J.

XX PA (DUFO/) DUFOURCO J.

XX PA (METZ/) METZ G.

XX PA (SEKU/) SEKUL R.

XX XX Buttner K, Cornut I, Dasseux J, Dufourcq J, Metz G;

XX XX Sekul R;

XX DR WPI; 1999-254921/21.

XX DR N-PSDB; AAX55971.

XX PT Nucleic acid encoding apolipoprotein A-I agonist peptides

XX PS Example; Fig 1; 232pp; English.

XX XX The present invention describes a nucleic acid (A) encoding an  
CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,  
CC which forms an amphipathic alpha-helix in presence of lipids. (A),  
CC optionally as a complex with lipids, and host cells that contain (A),  
CC are useful for gene therapy, or prevention, of diseases associated with  
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,  
CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I  
CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat  
CC endotoxemia (septic shock). Host cells containing (A) can also be used  
CC to study the role of apoA-I in lipid metabolism. (B) can be used  
CC diagnostically, e.g. to measure serum HDL (particularly its  
CC subpopulation involved in retrograde cholesterol transport) and for

CC imaging the circulatory system or HDL accumulations at fatty streaks.  
CC The present sequence represents human apoA-I.

SQ Sequence 267 AA;

Query Match 48.3%; Score 1024; DB 20; Length 267;

Best Local Similarity 88.5%; Pred. No. 2.5e-60;

Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 180 LEDLRQGLLPVLSFKVSLSALEEYTKKLTQGTGLKLDNDWDSVTSTFSKLRQGLGPTV 239  
Db 35 VKDLATVYVDLVKDSGRDYSQFE--GSALGKQLNLKLDNDWDSVTSTFSKLRQGLGPTV 92  
QY 240 QEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQ 299  
Db 93 QEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQ 152  
QY 300 GARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 359  
Db 153 GARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 212  
QY 360 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLSFKVSLSALEEYTKKLTQ 414  
Db 213 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLSFKVSLSALEEYTKKLTQ 267

## RESULT 7

AA47620  
ID AAB47620 standard; Protein; 267 AA.

XX AC AAB47620;

XX DT 21-JAN-2002 (first entry)

XX DE Full length Apo-A1.

XX KW Apolipoprotein; Apo-A1; Apo-A-I fragment T-cell activation inhibitor;  
KW AFTI; monocyte; IL-1; interleukin 1; TNF; tumour necrosis factor;  
KW acute pancreatitis; Alzheimer's disease; asthma; cancer; fever;  
KW inflammatory bowel disease; ischemia; multiple sclerosis; osteoporosis;  
KW Parkinson's disease; psoriasis; probe.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Binding-site 44..65

XX FT /label= Helical lipid binding domain

XX FT Binding-site 220..241

XX FT /label= Helical lipid binding domain

XX FT Domain 74..111

XX FT /note= "Involved in lipoprotein-mediated cholesterol

XX FT efflux from monocytes"

XX FT Binding-site 149..219

XX FT /label= Receptor binding domain

XX FT Domain 99..120

XX FT /label= Major antigenic epitope domain

XX FT Domain 99..143

XX FT /label= Hinged domain

XX FT Domain 66..120

XX FT /label= Phylogenetically conserved domain

XX FT Domain 90..111

XX FT /note= "Involved in lectin-cholesterol acyltransferase

XX FT activity"

XX FT Domain 44..65

XX FT /label= Amphipathic helix

XX FT Domain 66..98

XX FT /label= Amphipathic helix

XX FT Domain 99..120

XX FT /label= Amphipathic helix

XX FT Domain 121..142

XX FT /label= Amphipathic helix

XX FT Domain 143..164

XX FT /label= Amphipathic helix



[illegible]







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PD XX 25-OCT-2001.
PF XX 16-APR-2001; 2001WO-US08656.
PR XX 18-APR-2000; 2000US-0552929.
PR XX 26-JAN-2001; 2001US-0770160.
PA (HYSE-) HYSEQ INC.
XX XX
PI Tang YT, Liu C, Drmanac RT;
XX XX
DR WPI; 2001-611725/70.
XX XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX XX
PS Claim 20; Page 199; 765pp; English.
XX XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX XX
SQ Sequence 221 AA;

Query Match 37.2%; Score 788; DB 22; Length 221;
Best Local Similarity 99.4%; Pred. No. 8.3e-45;
Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 222 DSVTSTFKRLRQLGPTVQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFFQKKWQE 281
Db 66 DSVTSTFKRLRQLGPTVQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFFQKKWQE 125
QY 282 EMELYRQKVEPLRAELQEGARQKLHELOEKLSPGLGEEMRDRARAHVDALRTHLAPYSDEL 341
Db 126 EMELYRQKVEPLRAELQEGARQKLHELOEKLSPGLGEEMRDRARAHVDALRTHLAPYSDEL 185
QY 342 RORLAARLEALKENGARLAIEYHAKATEHLSTLSEK 377
Db 186 RORLAARLEALKENGARLAIEYHAKATEHLSTLSEK 221

RESULT 15
AAU30268
ID AAU30268 standard; Protein; 318 AA.
XX AC
XX AC AAU30268;
XX DT
XX DT 18-DEC-2001 (first entry)
XX DE
XX DE Novel human secreted protein #759.
XX KW
XX KW Human; vaccination; gene therapy; nutritional supplement;
XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200179449-A2.
XX XX

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PD XX 25-OCT-2001.
PF XX 16-APR-2001; 2001WO-US08656.
PR XX 18-APR-2000; 2000US-0552929.
PR XX 26-JAN-2001; 2001US-0770160.
PA (HYSE-) HYSEQ INC.
XX XX
PI Tang YT, Liu C, Drmanac RT;
XX XX
DR WPI; 2001-611725/70.
XX XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX XX
PS Claim 20; Page 270; 765pp; English.
XX XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX XX
SQ Sequence 318 AA;

Query Match 34.3%; Score 726.5; DB 22; Length 318;
Best Local Similarity 76.7%; Pred. No. 1.5e-40;
Matches 161; Conservative 12; Mismatches 28; Indels 9; Gaps 9;

QY 214 TLKLLDNW-DSVTSTFS-KLREOLGPTVQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPY 271
Db 84 TLKLLDNWGORXSPSTFQPSCAKQLGPTQEFWYNLEKETEGFRQEMSKDLEEVKAKVQPY 143
QY 272 -LDDFOKK-WQEMELYRQKVEPL-RAELQEGAR-QKLHEL-OEKLSPGLGEEM-RDRARA 325
Db 144 TLDDFOERSWQEMELYRQKVEPLARKNFQEGARPESLHELARRSLSPGLGEAVSRPRAP 203
QY 326 HVDALRTHLAPYSDELQRILA-ARLEALKENGARLAIEYHAKATEHLSTLSEKAKPALED 384
Db 204 MWDALRTHLAPYSDEMMPALGRAPICGALRENGGARMGQYHAQTHLSTLSEKAKPALED 263
QY 385 LROGLLPVLESFKVSFLSALEEYTKKLTNQ 414
Db 264 LROGLLPVLESFKVSFLSALEEYTKKLTNQ 293

Search completed: April 30, 2003, 15:11:43
Job time : 40 secs

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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 30, 2003, 15:11:02 ; Search time 18 Seconds  
(without alignments)  
676.727 Million cell updates/sec

Title: US-09-990-087-17  
Perfect score: 2118  
Sequence: 1 MGHHHHHIEGRLLDNWD.....SFKVSFLSALEETKTKINTQ 414

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents.AA:\*  
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4: /cgn2.6/ptodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2.6/ptodata/1/1aa/PTCUS\_COMB.pep.\*  
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1024	48.3	267	1	US-07-959-946-3
2	1024	48.3	267	1	US-08-333-577-3
3	1024	48.3	267	4	US-08-952-796-2
4	1024	48.3	267	5	PCT-US92-08634-3
5	1017	48.0	264	1	US-08-448-606-6
6	1006	47.5	200	4	US-08-952-796-15
7	328	15.5	64	2	US-08-292-870-1
8	227	10.7	44	2	US-08-292-870-2
9	216.5	10.2	366	4	US-09-750-580-3
10	198.5	9.4	2101	1	US-08-466-390-4
11	198.5	9.4	2101	1	US-08-470-950-4
12	198.5	9.4	2101	1	US-08-467-781-4
13	198.5	9.4	2101	1	US-08-195-487-4
14	198.5	9.4	2101	2	US-08-483-924-4
15	198.5	9.4	2101	4	US-09-452-294-1
16	198.5	9.4	2101	5	PCT-US93-06160-4
17	192.5	9.1	1939	4	US-09-310-187A-1
18	191.5	9.0	1886	4	US-08-938-105-3
19	190	9.0	534	4	US-09-103-664A-2
20	190	9.0	1184	4	US-09-541-782-2
21	190	9.0	1184	4	US-09-723-820-2
22	185.5	8.8	683	6	5210183-3
23	183.5	8.7	816	2	US-08-533-306A-6
24	183.5	8.7	816	2	US-08-742-923A-6
25	183.5	8.7	885	2	US-08-533-306A-4
26	183.5	8.7	885	2	US-08-742-923A-4
27	183	8.6	477	1	US-08-402-217A-3

28	183	8.6	477	1	US-08-700-178-3	Sequence 3, Appli
29	183	8.6	477	3	US-08-995-654-3	Sequence 3, Appli
30	182	8.6	606	4	US-08-477-831C-2	Sequence 2, Appli
31	182	8.6	631	4	US-08-477-831C-11	Sequence 11, Appli
32	181.5	8.6	3248	1	US-08-353-700-1	Sequence 1, Appli
33	181.5	8.6	3248	5	PCT-US95-16216-1	Sequence 1, Appli
34	180.5	8.5	2482	1	US-08-328-254-6	Sequence 6, Appli
35	179.5	8.5	317	4	US-08-949-155-6	Sequence 6, Appli
36	179.5	8.5	317	4	US-09-819-964-6	Sequence 6, Appli
37	175.5	8.3	803	4	US-09-154-750A-85	Sequence 85, Appli
38	175.5	8.3	1068	4	US-09-085-199B-11	Sequence 11, Appli
39	169.5	8.0	515	2	US-08-705-660-46	Sequence 46, Appli
40	169.5	8.0	515	3	US-08-989-045-46	Sequence 11, Appli
41	166	7.8	1588	5	PCT-US93-07261-11	Sequence 16, Appli
42	166	7.8	1663	5	PCT-US93-07261-16	Sequence 2, Appli
43	165	7.8	317	1	US-07-709-949-2	Sequence 2, Appli
44	163.5	7.7	1312	2	US-08-592-126-148	Sequence 148, App
45	163.5	7.7	1312	2	US-08-687-080-51	Sequence 51, Appli

ALIGNMENTS

RESULT 1  
US-07-959-946-3  
; Sequence 3, Application US/07959946  
; Patent No. 5408038  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Richard K.  
; APPLICANT: Koduri, Raju  
; APPLICANT: Young, Stephen G.  
; APPLICANT: Witzum, Joseph L.  
; APPLICANT: Curtiss, Linda K.  
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a  
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &  
; ADDRESSEE: Milnamow, Ltd.  
; STREET: 180 No. 5408038th Stetson, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/959,946  
; FILING DATE: 19921008  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,706  
; FILING DATE: 18-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ganson, Edward P.  
; REGISTRATION NUMBER: 29,381  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312)616-5400  
; TELEFAX: (312)616-5460  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-959-946-3

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Best Local Similarity 88.5%; Pred. No. 8.8e-67;

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Db	213	LAETHAKATEHLSTLSKAKPALEDLROGLLPVLESFKVSFLSALEYTKKLNTQ	267

RESULT 3  
 US-08-952-796-2  
   : Sequence 2, Application US/08952796  
   : Patent NO. 6258596  
   : GENERAL INFORMATION:  
   : APPLICANT: BENOIT, Patrick  
   : APPLICANT: BRUCKERT, Eric  
   : APPLICANT: DENEFFE, Patrice  
   : APPLICANT: DUBERGER, Nicolas  
   : APPLICANT: FRUCHART, Jean-Charles  
   : APPLICANT: LUC, Gerald  
   : APPLICANT: TURPIN, Gerard  
   : APPLICANT: ASSMANN, Gerd  
   : APPLICANT: FUNKE, Harald  
   : TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPOPROTEIN A-I  
   : NUMBER OF SEQUENCES: 19  
   : CORRESPONDENCE ADDRESS:  
   : ADDRESSEE: Rhone-Poulenc Rorer Inc.  
   : STREET: 500 Arcola Road, Mailstop 3c43  
   : CITY: Collegeville  
   : STATE: PA  
   : COUNTRY: USA  
   : ZIP: 19426  
   : COMPUTER READABLE FORM:  
   : MEDIUM TYPE: Floppy disk  
   : COMPUTER: IBM PC compatible  
   : OPERATING SYSTEM: PC-DOS/MS-DOS  
   : SOFTWARE: Patentin Release #1.0, Version #1.30  
   : CURRENT APPLICATION DATA: US/08/952,796  
   : FILING DATE:  
   : CLASSIFICATION: 424  
   : PRIOR APPLICATION DATA:  
   : APPLICATION NUMBER: FR 95/06061  
   : FILING DATE: 22-MAY-1995  
   : PRIOR APPLICATION DATA:  
   : APPLICATION NUMBER: WO FR96/00747  
   : FILING DATE: 20-MAY-1996  
   : ATTORNEY/AGENT INFORMATION:  
   : NAME: Fehlnert Esq., Paul F.  
   : REGISTRATION NUMBER: 35,135  
   : REFERENCE/DOCKET NUMBER: ST95031-US  
   : TELECOMMUNICATION INFORMATION:  
   : TELEPHONE: (610) 454-3839  
   : TELEFAX: (610) 454-3808  
   : INFORMATION FOR SEQ ID NO: 2:  
   : SEQUENCE CHARACTERISTICS:  
   : LENGTH: 267 amino acids  
   : TYPE: amino acid  
   : TOPOLOGY: linear  
   : MOLECULE TYPE: protein  
 US-08-952-796-2

	Query Match	48.3%;	Score 1024;	DB 4;	Length 267;
	Best Local Similarity	88.5%;	Pred. No. 8.8e-67;		
	Matches 208;	Conservative	6; Mismatches 19;	Indels	2; Gaps
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	:	: :	:	:	:
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QY 240 QEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQ 299  
Db 93 QEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQ 152  
QY 300 GARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELORLAARLEALKENGAR 359  
Db 153 GARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELORLAARLEALKENGAR 212  
QY 360 LAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNQ 414  
Db 213 LAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNQ 267

RESULT 4  
PCT-US92-08634-3  
; Sequence 3, Application PC/TUS9208634  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Richard K.  
; APPLICANT: Koduri, Raju  
; APPLICANT: Young, Stephen G.  
; APPLICANT: Witzum, Joseph L.  
; APPLICANT: Curtiss, Linda K.  
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a  
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Goldsmith, Shore, Sukter &  
; ADDRESSEE: Milnamow, Ltd.  
; STREET: 180 North Stetson, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/08634  
; FILING DATE: 19921009  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,706  
; FILING DATE: 18-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gamson, Edward P.  
; REGISTRATION NUMBER: 29,381  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312)616-5400  
; TELEFAX: (312)616-5460  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US92-08634-3

Query Match 48.3%; Score 1024; DB 5; Length 267;  
Best Local Similarity 88.5%; Pred. No. 8.8e-67;  
Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;  
QY 180 LEDRQGLLPVLESFKVSFLSALEEYTKKLNQGTGLKLDNWDVSTFSKLEQLGPGVT 239  
Db 35 VKDLATVYDVLDKSGRDYVSQFE--GSALGKQLNLKLDNWDVSTFSKLEQLGPGVT 92  
QY 240 QEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQ 299  
Db 93 QEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQ 152  
QY 300 GARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELORLAARLEALKENGAR 359

Db 153 GARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELORLAARLEALKENGAR 212  
QY 360 LAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNQ 414  
Db 213 LAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNQ 267

RESULT 5  
US-08-448-606-6  
; Sequence 6, Application US/08448606  
; Patent No. 5721114  
; GENERAL INFORMATION:  
; APPLICANT: Abrahams n, Lars  
; APPLICANT: Holmgren, Erik  
; APPLICANT: Kalder n, Christina  
; APPLICANT: Lake, Mats  
; APPLICANT: Mikaelsson, sa  
; APPLICANT: Sejlitz, Torsten  
; TITLE OF INVENTION: Expression System For Producing  
; TITLE OF INVENTION: Apolipoprotein AI-M  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pollock, Vande Sande & Priddy  
; STREET: 1990 M Street, N.W., Suite 800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,606  
; FILING DATE: 25-AUG-1995  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/SE93/01061  
; FILING DATE: 09-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: SE 9203753-0  
; FILING DATE: 11-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amernick, Burton A.  
; REGISTRATION NUMBER: 24,852  
; REFERENCE/DOCKET NUMBER: 0151/00121  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)331-7111  
; TELEFAX: (202) 293-6229  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 264 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-448-606-6

Query Match 48.0%; Score 1017; DB 1; Length 264;  
Best Local Similarity 81.8%; Pred. No. 2.8e-66;  
Matches 211; Conservative 10; Mismatches 29; Indels 8; Gaps 2;  
QY 163 AKATEHLSTLSEKAKP-----ALEDLRQGLLPVLESFKVSFLSALEEYTKKLNQGTGLK 216  
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QY 217 LLDNWDVSTFSKLEQLGPGVTQEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQ 276  
Db 67 LLDNWDVSTFSKLEQLGPGVTQEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQ 126  
QY 277 KWKQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAP 336

Db 127 KKQWEEMLYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAP 186  
QY 337 YSELRORLAARLEALKENGARLAIEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESF 396  
Db 187 YSELROCLAARLEALKENGARLAIEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESF 246  
QY 397 KVSFLSALEEYTKKLNQ 414  
Db 247 KVSFLSALEEYTKKLNQ 264  
RESULT 6  
US-08-952-796-15  
; Sequence 15, Application US/08952796  
; Patent No. 6258596  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: BRUCKERT, Eric  
; APPLICANT: DENEFLER, Patrice  
; APPLICANT: DUBERGER, Nicolas  
; APPLICANT: FRUCHART, Jean-Charles  
; APPLICANT: LUC, Gerald  
; APPLICANT: TURPIN, Gerard  
; APPLICANT: ASSMANN, Gerd  
; APPLICANT: FUNKE, Harald  
; TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPOPROTEIN A-I  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, Mailstop 3c43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/952,796  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95/06061  
; FILING DATE: 22-MAY-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO FR96/00747  
; FILING DATE: 20-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fehlnert Esq., Paul F.  
; REGISTRATION NUMBER: 35,135  
; REFERENCE/DOCKET NUMBER: ST95031-US  
; TELEPHONE: (610) 454-3839  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 200 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-952-796-15  
Query Match 47.5%; Score 1006; DB 4; Length 200;  
Best Local Similarity 99.5%; Pred. No. 1,2e-65;  
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 1 LKLLDNWDSVSTFSKLEQGLPVTQEFWDNLEKETEGRLQEMSKDLFEVAKVQPYLDD 60  
QY 275 FOKKQWEEMLYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHL 334

Db 61 FOKKQWEEMLYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHL 120  
QY 335 APYSELQRLAARLEALKENGARLAIEYHAKATEHLSTLSEKAKPALEDLROGLLPVLE 394  
Db 121 APYSELQRLAARLEALKENGARLAIEYHAKATEHLSTLSEKAKPALEDLROGLLPVLE 180  
QY 395 SPKVSFLSALEEYTKKLNQ 414  
Db 181 SPKVSFLSALEEYTKKLNQ 200  
RESULT 7  
US-08-292-870-1  
; Sequence 1, Application US/08292870  
; Patent No. 5814467  
; GENERAL INFORMATION:  
; APPLICANT: Curtiss, Linda K  
; APPLICANT: Banka, Carole L  
; APPLICANT: Bonnet, David J  
; APPLICANT: Smith, Richard S  
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS  
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 581467th Torrey Pines Road., TPC 8  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,870  
; FILING DATE: 17-AUG-1994  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/534,761  
; FILING DATE: 07-JUN-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/711,333  
; FILING DATE: 06-JUN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US 91/04038  
; FILING DATE: 07-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 64 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-292-870-1  
Query Match 15.5%; Score 328; DB 2; Length 64;  
Best Local Similarity 100.0%; Pred. No. 2.2e-17;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 256 EMSKDLFEVAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPL 315

Db 1 EMSKDLVEKAKVQPYLDQFKKQWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPL 60

QY 316 GEEM 319  
|||||

Db 61 GEEM 64

RESULT 8

US-08-292-870-2

Sequence 2, Application US/08292870

Patent No. 5814467

GENERAL INFORMATION:

APPLICANT: Curtiss, Linda K

APPLICANT: Banka, Carole L

APPLICANT: Bonnet, David J

APPLICANT: Smith, Richard S

TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS

TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8

CITY: La Jolla

STATE: California

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/292,870

FILING DATE: 17-AUG-1994

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/534,761

FILING DATE: 07-JUN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/711,333

FILING DATE: 06-JUN-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US 91/04038

FILING DATE: 07-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 210.1 D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-292-870-2

Query Match 10.7%; Score 227; DB 2; Length 44;

Best Local Similarity 100.0%; Pred. No. 2.6e-10;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 ROEMSKDLVEKAKVQPYLDQFKKQWQEMELYRQKVEPLRAEL 297

Db 1 ROEMSKDLVEKAKVQPYLDQFKKQWQEMELYRQKVEPLRAEL 44

RESULT 9

US-09-750-580-3

Sequence 3, Application US/09750580

Patent No. 6455280

GENERAL INFORMATION:

APPLICANT: Yen, Frances

APPLICANT: Denison, Blake

APPLICANT: Bour, Barbara

APPLICANT: Bihain, Bernard

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Duclert, Aymeric

APPLICANT: Bougueleret, Lydie

APPLICANT: Ebbets-Reed, Dana

APPLICANT: Salter-Cld, Luisa

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH

FILE REFERENCE: 89 US2 CIP

CURRENT APPLICATION NUMBER: US/09/750,580

CURRENT FILING DATE: 2000-12-28

PRIOR APPLICATION NUMBER: US 09/599,362

PRIOR FILING DATE: 2000-06-21

PRIOR APPLICATION NUMBER: PCT/IB00/0101

PRIOR FILING DATE: 2000-06-21

PRIOR APPLICATION NUMBER: PCT/IB99/02058

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: US 49/469/099

PRIOR FILING DATE: 1999-12-21

PRIOR APPLICATION NUMBER: US 60/113,686

PRIOR FILING DATE: 1998-12-22

PRIOR APPLICATION NUMBER: US 60/141,032

PRIOR FILING DATE: 1999-06-25

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patent.pm

SEQ ID NO 3

LENGTH: 366

TYPE: PRT

ORGANISM: Homo sapiens

US-09-750-580-3

Query Match 10.2%; Score 216.5; DB 4; Length 366;

Best Local Similarity 23.0%; Pred No. 1.9e-08;

Matches 78; Conservative 68; Mismatches 136; Indels 57; Gaps 9;

QY 15 LLDNWDVSTFSLKREQLGPGVTFQFMDNLEKETGLRQEMSKDLVEKAKVQPYLDQFQ 74

Db 56 LKDSLEQDLNNMNFLEKRLPLSGSEAPRLQDPVGMRRQLQEELEEVKARLQPTMAEAH 115

QY 75 KKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMR-----DRAAHYDA 127

Db 116 ELVGNLEGLRQQLPYTMDLMEQVALRVQELQELRVVGEDTKAQLLGGVDAAWALLQG 175

QY 128 LRTHLAPYSDELQRQRLAARLEAKENGARLAHYHAKATEHLSTLSEKAKPALEDLRQGL 187

Db 176 LQSRVVHHTGRFKELFHPYAESLSVSGIGHVQELHRSVAPH-----APASPA----- 222

QY 188 LPVLESFKVSFLSALEETTKLNTQGTLLKLDNWDVSTFSLKREQLGPGVTFQFMDNLE 247

Db 223 -----RLSRCVQVLSRKLTLKAKALHARIOQNLQDLREEL---SRAFAGTGT 266

QY 248 KETGLRQEMSKDLVEKAKVQPYLDQ-----FQKQWQEMELYRQKVEP-----L 293

Db 267 EEGAGDPQMLSL--EEVRQRLQAFQDQTYLQTAAFRAIDQETEEVQOQLAPPPPGHSAF 324

QY 294 RAELOEGARQK-LHELQEKLSPLGEE---MRDRARAHV 327

Db 325 APEFOQDTSQKVLKQLARLDDLWEDITHSLHDQGHSHL 363

RESULT 10

US-08-466-390-4

Sequence 4, Application US/08466390

Patent No. 5686562

GENERAL INFORMATION:

APPLICANT: TOURKATLY, GARY

APPLICANT: LIDGARD, GRAHAM P

TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE

;; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX  
;; NUMBER OF SEQUENCES: 6  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
;; STREET: 125 HIGH STREET  
;; CITY: BOSTON  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02110  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/466,390  
;; FILING DATE: 06-JUN-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: PITCHER ESO, EDMUND R  
;; REGISTRATION NUMBER: 27,829  
;; REFERENCE/DOCKET NUMBER: MTP-013  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 248-7000  
;; TELEFAX: (617) 248-7100  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2101 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-466-390-4

Query Match 9.4%; Score 198.5; DB 1; Length 2101;  
Best Local Similarity 24.7%; Pred. No. 3e-06;  
Matches 95; Conservative 67; Mismatches 139; Indels 83; Gaps 16;  
QY 27 SKLRQLGPVTQEFWDLNLEKETEGRLQEMSKDLE-----EVKAKVQPYLDDFQKK 76  
Db 594 ASLRER-----DAALKQLEALEKEKAKELEILQOQLQVANEARDSAQTSVTQAR- 643  
QY 77 WOEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLEGEEMDRARAHVDALRTHLAPYS 136  
Db 644 --EKAELSR-KVEELQA-CVETARQEQHEAQVALEQLRSEQQKATE--KERVAQEK 697  
QY 137 DELRORLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKV 196  
Db 698 DQLQEQQLALKESLKVTKGS-LEEKKRAADAL-----EEQRCISELKAETRSVLEQHKR 752  
QY 197 SFLSALEEYTKLNTQGTLLKLDNWDVSTFSLRQLGPVTQEFWDLNLEKETEGRLQ 256  
b 753 ERKELEERAGRKGLERLL-----QLGEAHQ-----AETEVLRR 788  
QY 257 MSK-----DLEEVKAKVQPYLDDFQKKWQEME---LYRQKVEPLRAELQEGARQ 303  
Db 789 LAEAMAAQHTAESECEQLVKEVAWRDGYEDSQEQEAQYGAMFQEQMLTKKEC-EKARQ 847  
QY 304 KLHELOEKLS-----PLGEEMDRARAHVDALRTHLAPYSDELRL-ORLAARLEALKE 354  
Db 848 ELQEAKEKVAGIESHSELQISROQNKLAELHANLARALQOQVEKVRQAQLDADLSTLQ 907  
QY 355 NGGARLAHYHAKATEHLSTLSEKA 378  
Db 908 KMAAT-----SKEVARLETLLVRKA 926

RESULT 11  
US-08-470-950-4  
; Sequence 4, Application US/08470950  
; Patent No. 5698439  
; GENERAL INFORMATION:  
; APPLICANT: TOUKATLY, GARY  
; APPLICANT: LIDGARD, GRAHAM P

;; TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE  
;; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX  
;; NUMBER OF SEQUENCES: 6  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
;; STREET: 125 HIGH STREET  
;; CITY: BOSTON  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02110  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/470,950  
;; FILING DATE: 06-JUN-1995  
;; CLASSIFICATION: 536  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: PITCHER ESO, EDMUND R  
;; REGISTRATION NUMBER: 27,829  
;; REFERENCE/DOCKET NUMBER: MTP-013  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 248-7000  
;; TELEFAX: (617) 248-7100  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2101 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-470-950-4

Query Match 9.4%; Score 198.5; DB 1; Length 2101;  
Best Local Similarity 24.7%; Pred. No. 3e-06;  
Matches 95; Conservative 67; Mismatches 139; Indels 83; Gaps 16;  
QY 27 SKLRQLGPVTQEFWDLNLEKETEGRLQEMSKDLE-----EVKAKVQPYLDDFQKK 76  
Db 594 ASLRER-----DAALKQLEALEKEKAKELEILQOQLQVANEARDSAQTSVTQAR- 643  
QY 77 WOEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLEGEEMDRARAHVDALRTHLAPYS 136  
Db 644 --EKAELSR-KVEELQA-CVETARQEQHEAQVALEQLRSEQQKATE--KERVAQEK 697  
QY 137 DELRORLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKV 196  
Db 698 DQLQEQQLALKESLKVTKGS-LEEKKRAADAL-----EEQRCISELKAETRSVLEQHKR 752  
QY 197 SFLSALEEYTKLNTQGTLLKLDNWDVSTFSLRQLGPVTQEFWDLNLEKETEGRLQ 256  
Db 753 ERKELEERAGRKGLERLL-----QLGEAHQ-----AETEVLRR 788  
QY 257 MSK-----DLEEVKAKVQPYLDDFQKKWQEME---LYRQKVEPLRAELQEGARQ 303  
Db 789 LAEAMAAQHTAESECEQLVKEVAWRDGYEDSQEQEAQYGAMFQEQMLTKKEC-EKARQ 847  
QY 304 KLHELOEKLS-----PLGEEMDRARAHVDALRTHLAPYSDELRL-ORLAARLEALKE 354  
Db 848 ELQEAKEKVAGIESHSELQISROQNKLAELHANLARALQOQVEKVRQAQLDADLSTLQ 907  
QY 355 NGGARLAHYHAKATEHLSTLSEKA 378  
Db 908 KMAAT-----SKEVARLETLLVRKA 926

RESULT 12  
US-08-467-781-4  
; Sequence 4, Application US/08467781  
; Patent No. 5780596  
; GENERAL INFORMATION:  
; APPLICANT: TOUKATLY, GARY



```

; APPLICANT: LIDGARD, GRAHAM P
; TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,781
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESO, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MTP-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2101 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-781-4

Query Match          9.4%; Score 198.5; DB 1; Length 2101;
Best Local Similarity 24.7%; Pred. No. 3e-06;
Matches 95; Conservative 67; Mismatches 139; Indels 83; Gaps 16;

QY 27 SKLRQLGVPVTFQFWDNLEKETGLRQEMSKDLE-----EVKAKVPYLDLDFQKK 76
Db 594 ASLSR-----DAALKQLEALEKEKAALKLEILQOQLQVANEARDSAQTSVTOAQR- 643

QY 77 WOEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGEMMRDRARAHVDALRTHLAPYS 136
Db 644 --EKAELSR-KVEELQA-CVETARQOEHAQAQVAELEQLRSEQQKATE--KERVQAEK 697

QY 137 DELRQRLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKV 196
Db 698 DQLQEQALQALKESLVKTKGS-LEEKKRAADAL-----EEQRCISSELKAETRSILVEQHKR 752

QY 197 SFLSALAEYTKKLTNQTGTLKLLDNWDSVTSTFSKLRLQGLPVPTQFWDNLEKETGLRQ 256
Db 753 ERKELEERAGRKGLAEARLL-----OLGEAHQ-----AETEVLRRE 788

QY 257 MSK-----DLEEVKAKVPYLDLDFQKKQWEE-----LYRQKVEPLRAELQEGARQ 303
Db 789 LAEAMAAQHTAESECEQLVKVEAAWRDGYEDSQOEQAQYGMFQEQMLTKKEC-EKARQ 847

QY 304 KLHELOEKL-----PLGEMMRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKE 354
Db 848 ELQEAKEKVGAGIESHSELQISROONKLAELHANLARALQOQVEKRAQKLADLSTLQ 907

QY 355 NGGARLAHYHAKATEHLSTLSEKA 378
Db 908 KMAAT-----SKEVARLETIVRKA 926

RESULT 13
US-08-195-487-4
; Sequence 4, Application US/08195487
; Patent No. 5783403
; GENERAL INFORMATION:

```

```

; APPLICANT: TOUKATLY, GARY
; APPLICANT: LIDGARD, GRAHAM P
; TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,487
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/901,701
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MTP-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2101 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-195-487-4

Query Match          9.4%; Score 198.5; DB 1; Length 2101;
Best Local Similarity 24.7%; Pred. No. 3e-06;
Matches 95; Conservative 67; Mismatches 139; Indels 83; Gaps 16;

QY 27 SKLRQLGVPVTFQFWDNLEKETGLRQEMSKDLE-----EVKAKVPYLDLDFQKK 76
Db 594 ASLSR-----DAALKQLEALEKEKAALKLEILQOQLQVANEARDSAQTSVTOAQR- 643

QY 77 WOEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGEMMRDRARAHVDALRTHLAPYS 136
Db 644 --EKAELSR-KVEELQA-CVETARQOEHAQAQVAELEQLRSEQQKATE--KERVQAEK 697

QY 137 DELRQRLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKV 196
Db 698 DQLQEQALQALKESLVKTKGS-LEEKKRAADAL-----EEQRCISSELKAETRSILVEQHKR 752

QY 197 SFLSALAEYTKKLTNQTGTLKLLDNWDSVTSTFSKLRLQGLPVPTQFWDNLEKETGLRQ 256
Db 753 ERKELEERAGRKGLAEARLL-----OLGEAHQ-----AETEVLRRE 788

QY 257 MSK-----DLEEVKAKVPYLDLDFQKKQWEE-----LYRQKVEPLRAELQEGARQ 303
Db 789 LAEAMAAQHTAESECEQLVKVEAAWRDGYEDSQOEQAQYGMFQEQMLTKKEC-EKARQ 847

QY 304 KLHELOEKL-----PLGEMMRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKE 354
Db 848 ELQEAKEKVGAGIESHSELQISROONKLAELHANLARALQOQVEKRAQKLADLSTLQ 907

QY 355 NGGARLAHYHAKATEHLSTLSEKA 378
Db 908 KMAAT-----SKEVARLETIVRKA 926

RESULT 14

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US-08-483-924-4  
; Sequence 4, Application US/08483924  
; Patent No. 5882876  
; GENERAL INFORMATION:  
; APPLICANT: TOURATLY, GARY  
; APPLICANT: LIDGARD, GRAHAM P  
; TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE  
; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
; STREET: 125 HIGH STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/483,924  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PITCHER ESO, EDMUND R  
; REGISTRATION NUMBER: 27,829  
; REFERENCE/DOCKET NUMBER: MTP-013  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2101 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-924-4

Query Match 9.4%; Score 198.5; DB 2; Length 2101;  
Best Local Similarity 24.7%; Pred. No. 3e-06;  
Matches 95; Conservative 67; Mismatches 139; Indels 83; Gaps 16;  
QY 27 SKLREQLGVPVTOEFWDNLEKETEGLRQEMSKDLE-----EVKAKVQPYLDDDFQKK 76  
Db 594 ASLRR-----DAALKQLEALEKEKALEILQOQLOVANEARDSAQTSTVQAQR- 643  
QY 77 WOEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYS 136  
Db 644 --EKAELSR-KVEELQA-CVETARQEQHEAQAQVAELELQRLSEQQKATE--KERVAQEK 697  
QY 137 DELRQRLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKV 196  
Db 698 DQLOEQLOALKESLKVTKGS-LEEKRRADAL-----EQQRCSISELKAEATRSLSVQHKR 752  
QY 197 SFLSALAEYTKKLTQGTGLKLDNWDVSTFTSKLREQLGVPVTOEFWDNLEKETEGLRQE 256  
Db 753 ERKELEERAGRKGLEARLL-----QLGEAHQ-----AETEVLRRE 788  
QY 257 MSK-----DLEEVKAKVQPYLDDDFQKKWQEME---LYRQKVEPLRAELQEGARQ 303  
Db 789 LAEAMAAQHTAESECEQLVKEVAAWRDGYEDSQEEAQYGAMFQQLMTLKEEC-EKARQ 847  
QY 304 KLHELQEKLS-----PLGEMRDRARAHVDALRTHLAPYSDELRL-ORLAARLEALKE 354  
Db 848 ELQEAKEKVAGIESHSELQISROQNKLAELHANLARALQOQVEKVRQAQKLADDLSTLQE 907  
QY 355 NGGARLAHYHAKATEHLSTLSEKA 378  
Db 908 KMAAT-----SKEVARLETIVRKA 926

Search completed: April 30, 2003, 15:14:33  
Job time : 23 secs

RESULT 15  
US-09-452-294-1  
; Sequence 1, Application US/09452294  
; Patent No. 6287790  
; GENERAL INFORMATION:  
; APPLICANT: Lelievre, Sophie  
; APPLICANT: Bissell, Mina  
; TITLE OF INVENTION: UTILIZATION OF NUCLEAR STRUCTURAL PROTEINS FOR TARGETED  
; TITLE OF INVENTION: THERAPH AND DETECTION OF PROLIFERATIVE AND  
; TITLE OF INVENTION: DIFFERENTIATION DISORDERS  
; FILE REFERENCE: IB-1454- Sequence Submittal  
; Patent No. 6287790  
; CURRENT APPLICATION NUMBER: US/09/452,294  
; CURRENT FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: 60/110,420  
; PRIOR FILING DATE: 1998-11-30  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2101  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-452-294-1

Query Match 9.4%; Score 198.5; DB 4; Length 2101;  
Best Local Similarity 24.7%; Pred. No. 3e-06;  
Matches 95; Conservative 67; Mismatches 139; Indels 83; Gaps 16;  
QY 27 SKLREQLGVPVTOEFWDNLEKETEGLRQEMSKDLE-----EVKAKVQPYLDDDFQKK 76  
Db 594 ASLRR-----DAALKQLEALEKEKALEILQOQLOVANEARDSAQTSTVQAQR- 643  
QY 77 WOEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYS 136  
Db 644 --EKAELSR-KVEELQA-CVETARQEQHEAQAQVAELELQRLSEQQKATE--KERVAQEK 697  
QY 137 DELRQRLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKV 196  
Db 698 DQLOEQLOALKESLKVTKGS-LEEKRRADAL-----EQQRCSISELKAEATRSLSVQHKR 752  
QY 197 SFLSALAEYTKKLTQGTGLKLDNWDVSTFTSKLREQLGVPVTOEFWDNLEKETEGLRQE 256  
Db 753 ERKELEERAGRKGLEARLL-----QLGEAHQ-----AETEVLRRE 788  
QY 257 MSK-----DLEEVKAKVQPYLDDDFQKKWQEME---LYRQKVEPLRAELQEGARQ 303  
Db 789 LAEAMAAQHTAESECEQLVKEVAAWRDGYEDSQEEAQYGAMFQQLMTLKEEC-EKARQ 847  
QY 304 KLHELQEKLS-----PLGEMRDRARAHVDALRTHLAPYSDELRL-ORLAARLEALKE 354  
Db 848 ELQEAKEKVAGIESHSELQISROQNKLAELHANLARALQOQVEKVRQAQKLADDLSTLQE 907  
QY 355 NGGARLAHYHAKATEHLSTLSEKA 378  
Db 908 KMAAT-----SKEVARLETIVRKA 926

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 30, 2003, 15:13:43 ; Search time 47 Seconds  
(without alignments)  
760.057 Million cell updates/sec

Title: US-09-990-087-17  
Perfect score: 2118  
Sequence: 1 MGHSHHHHIEGRKLKLDND.....SFKVSFSLAEYTKKLNQ 414

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pap.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pap.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pap.\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pap.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pap.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pap.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1065	50.3	336	9	US-09-987-107-44
2	1063.5	50.2	337	9	US-09-987-107-46
3	1057	49.9	324	9	US-09-987-107-62
4	1056	49.9	316	9	US-09-987-107-48
5	1056	49.9	324	9	US-09-987-107-64
6	1051	49.6	316	9	US-09-987-107-54
7	1051	49.6	324	9	US-09-987-107-66
8	1049.5	49.6	323	9	US-09-987-107-58
9	1047.5	49.5	323	9	US-09-987-107-56
10	1045.5	49.4	323	9	US-09-987-107-60
11	1042	49.2	304	9	US-09-987-107-8
12	1041	49.2	304	9	US-09-987-107-7
13	1039.5	49.1	261	9	US-09-987-107-52
14	1038	49.0	304	9	US-09-987-107-6
15	1036.5	48.9	301	9	US-09-987-107-5
16	1036	48.9	306	9	US-09-987-107-9
17	1035.5	48.9	301	9	US-09-987-107-3
18	1034	48.8	306	9	US-09-987-107-11
19	1034	48.8	344	9	US-09-987-107-68

20	1033	48.8	306	9	US-09-987-107-10	Sequence 10, Appl
21	1031.5	48.7	273	9	US-09-987-107-50	Sequence 50, Appl
22	1029	48.6	258	9	US-09-987-107-4	Sequence 4, Appl
23	1024	48.3	243	9	US-09-987-107-1	Sequence 1, Appl
24	1024	48.3	244	9	US-09-987-107-2	Sequence 2, Appl
25	1024	48.3	267	9	US-09-987-107-15	Sequence 15, Appl
26	1024	48.3	267	9	US-09-802-640-30	Sequence 30, Appl
27	1024	48.3	267	10	US-09-803-918A-2	Sequence 2, Appl
28	1024	48.3	329	9	US-09-987-107-14	Sequence 14, Appl
29	991.5	46.8	267	9	US-09-987-107-16	Sequence 16, Appl
30	860.5	40.6	266	9	US-09-987-107-19	Sequence 19, Appl
31	837	39.5	266	9	US-09-987-107-20	Sequence 20, Appl
32	814	38.4	265	9	US-09-987-107-18	Sequence 18, Appl
33	798	37.7	265	9	US-09-987-107-17	Sequence 17, Appl
34	701.5	33.1	265	9	US-09-987-107-21	Sequence 21, Appl
35	668	31.5	170	10	US-09-803-918A-3	Sequence 3, Appl
36	653	30.8	264	9	US-09-987-107-22	Sequence 22, Appl
37	614	29.0	241	9	US-09-987-107-24	Sequence 24, Appl
38	584	27.6	259	9	US-09-987-107-23	Sequence 23, Appl
39	505.5	23.9	264	9	US-09-987-107-27	Sequence 27, Appl
40	491.5	23.2	264	9	US-09-987-107-25	Sequence 25, Appl
41	470.5	22.2	264	9	US-09-987-107-26	Sequence 26, Appl
42	350.5	16.5	429	9	US-09-987-107-34	Sequence 34, Appl
43	339.5	16.0	401	9	US-09-987-107-36	Sequence 36, Appl
44	324.5	15.3	396	10	US-09-800-729-207	Sequence 207, Appl
45	320.5	15.1	396	9	US-09-987-107-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1  
US-09-987-107-44  
; Sequence 44, Application US/09987107  
; Patent No. US20020156007A1  
; GENERAL INFORMATION:  
; APPLICANT: GRAVERSEN, Jonas  
; APPLICANT: MOESTRUP, Soren  
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES  
; FILE REFERENCE: GRAVERSENIA  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/264,022  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: DK PA2001 00057  
; PRIOR FILING DATE: 2001-01-15  
; PRIOR APPLICATION NUMBER: DK PA2000 01682  
; PRIOR FILING DATE: 2000-11-10  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 44  
; LENGTH: 336  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pT7 H6ubiF Apo A-1 plasmid  
US-09-987-107-44  
Query Match 50.3%; Score 1065; DB 9; Length 336;  
Best Local Similarity 57.7%; Pred. No. 2.8e-53;  
Matches 240; Conservative 27; Mismatches 67; Indels 82; Gaps 7;  
QY 1 MGHSHHHHIEGRKLKLDNDSDVTSFSLAEYTKKLNQKLTLEVEPSDRIE 60  
Db 1 MGHSHHHH-HG-----SQIFVTKLTGKTTITLEVEPSDRIE 34  
QY 61 EVKAKYQPYLDDFQKKWOEMELYRQKVEPLRAELQEGAROKLHELQELKSLPLGEMDRDR 120  
Db 35 NVKAKIQD-----KGIIPDQQRLLIFAGKQLEDGRTLSYDNIQ-KESTLHLVLKLR 84  
QY 121 ARAHVDALETHLAPYS--DELQRQLAARLEALKENGARLAIEYHAKATEHLSTLSEKAKP 178  
Db 85 G-GSIEGRGGDEPPQSPQPMWRVKDLATVYVDLKDSDRDVVSQFEGSA----- 130

QY 179 ALEDLROGLLPVLESFKVSVLSALEEYTKKLTQGTGTLKLLDNWDSVTSTFSKLRQGLGPV 238  
Db 131 -----LGKQLNKLKLLDNWDSVTSTFSKLRQGLGPV 160  
QY 239 TQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDLDFQKKWQOEEMELYRQKVEPLRAELQ 298  
Db 161 TQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDLDFQKKWQOEEMELYRQKVEPLRAELQ 220  
QY 299 EGARQKHELOEKLSPGEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEAKENGGA 358  
Db 221 EGARQKHELOEKLSPGEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEAKENGGA 280  
QY 359 RLAEYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSVLSALEEYTKKLTQ 414  
Db 281 RLAEYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSVLSALEEYTKKLTQ 336

RESULT 2  
US-09-987-107-46  
; Sequence 46, Application US/09987107  
; Patent No. US20020156007A1  
; GENERAL INFORMATION:  
; APPLICANT: GRAVERSEN, Jonas  
; APPLICANT: MOESTRUP, Soren  
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES  
; FILE REFERENCE: GRAVERSENIA  
; CURRENT APPLICATION NUMBER: US/09/987,107  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: DK PA2001 00057  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: DK PA2000 01682  
; PRIOR FILING DATE: 2000-11-10  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 46  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: T7 H6b1fx Cys-Apo A-1 plasmid  
US-09-987-107-46

Query Match 50.2%; Score 1063.5; DB 9; Length 337;  
Best Local Similarity 57.5%; Pred. No. 3.4e-53;  
Matches 242; Conservative 25; Mismatches 63; Indels 91; Gaps 8;

QY 1 MGHSHHHH-HG-----SQIFVKTLTGKTTITLEVEPSDTIE 34  
Db 1 MGSHHHHH-HG-----SQIFVKTLTGKTTITLEVEPSDTIE 34  
QY 61 EVKAKVQPYLDLDFQKKWQOEEMELYRQKVEPLRAELQEGARQKHELOEKLSPGEMRDR 120  
Db 35 NVKAKID-----KEGIPPDQQLIFAGQLEDGRTLSYNIQ-KESTLHLVLRLR 84  
QY 121 -----ARAHVDALRTHLAPYS-DELRLQRLAARLEAKENGARLAHYHAKATEHLSLTS 173  
Db 85 GSGTEGRGCGDE-----PPQSPWDRVKDLATVYVDLKDGRDYVSQFEGSA----- 131  
QY 174 EKAKPALEDLROGLLPVLESFKVSVLSALEEYTKKLTQGTGTLKLLDNWDSVTSTFSKLR 233  
Db 132 -----LGKQLNKLKLLDNWDSVTSTFSKLR 156  
QY 234 QLGVPVTOEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDLDFQKKWQOEEMELYRQKVEPL 293  
Db 157 QLGVPVTOEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDLDFQKKWQOEEMELYRQKVEPL 216  
QY 294 RAELOEGARQKHELOEKLSPGEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEAK 353  
Db 217 RAELOEGARQKHELOEKLSPGEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEAK 276

QY 354 ENGARLAHYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSVLSALEEYTKKLT 413  
Db 277 ENGARLAHYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSVLSALEEYTKKLT 336  
QY 414 Q 414  
Db 337 Q 337

RESULT 3  
US-09-987-107-62  
; Sequence 62, Application US/09987107  
; Patent No. US20020156007A1  
; GENERAL INFORMATION:  
; APPLICANT: GRAVERSEN, Jonas  
; APPLICANT: MOESTRUP, Soren  
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES  
; FILE REFERENCE: GRAVERSENIA  
; CURRENT APPLICATION NUMBER: US/09/987,107  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/264,022  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: DK PA2001 00057  
; PRIOR FILING DATE: 2001-01-15  
; PRIOR APPLICATION NUMBER: DK PA2000 01682  
; PRIOR FILING DATE: 2000-11-10  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 62  
; LENGTH: 324  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pT7H6 (GS)3 Trip-A-Tn-Apo A1 AmpR plasmid  
US-09-987-107-62

Query Match 49.9%; Score 1057; DB 9; Length 324;  
Best Local Similarity 56.3%; Pred. No. 7.6e-53;  
Matches 238; Conservative 33; Mismatches 44; Indels 108; Gaps 11;

QY 1 MGHSHHHH-----IEGRKLKLLDNWDSVTSTFSKLRQGLGPVTOEFWDLNLEKETEGLRQ 53  
Db 1 MGSHHHHHSGSGSIQGRSPGTE-----PPTQK-----PKKIVNAKK 38  
QY 54 EM--SKDLEEVKAKVQPYLDLDFQKKWQOEEMELYRQKVEPLRAELQEGARQKHELOEKL 111  
Db 39 DVVNTKMPPELKS-----LDTL---AQEVALLEKQ-QALQTVSLKGS--KVHMKPEPPQS 87  
QY 112 PLGEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEAKENGARLAHYHAKATEHLSL 171  
Db 88 P-WDRVKDLATVYVD-----VLKDSGRDYVSQFEGSA----- 118  
QY 172 LSEKAKPALEDLROGLLPVLESFKVSVLSALEEYTKKLTQGTGTLKLLDNWDSVTSTFSKL 231  
Db 119 -----LGKQLNKLKLLDNWDSVTSTFSKL 141  
QY 232 RQGLGPVTOEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDLDFQKKWQOEEMELYRQKVE 291  
Db 142 RQGLGPVTOEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDLDFQKKWQOEEMELYRQKVE 201  
QY 292 PLRAELOEGARQKHELOEKLSPGEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEA 351  
Db 202 PLRAELOEGARQKHELOEKLSPGEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEA 261  
QY 352 LKENGARLAHYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSVLSALEEYTKKL 411  
Db 262 LKENGARLAHYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSVLSALEEYTKKL 321  
QY 412 NTQ 414  
Db 322 NTQ 324

## RESULT 4

US-09-987-107-48  
; Sequence 48, Application US/09987107  
; Patent No. US20020156007A1  
; GENERAL INFORMATION:  
; APPLICANT: GRAVERSEN, Jonas  
; APPLICANT: MOESTRUP, Soren  
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES  
; FILE REFERENCE: GRAVERSENIA  
; CURRENT APPLICATION NUMBER: US/09/987,107  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/264,022  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR FILING DATE: 2001-01-15  
; PRIOR APPLICATION NUMBER: DK PA2001 00057  
; PRIOR APPLICATION NUMBER: DK PA2000 01682  
; PRIOR FILING DATE: 2000-11-10  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 48  
; LENGTH: 316  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pT7 H6 Trip-A-Apo A-1 - AmpR plasmid  
US-09-987-107-48

Query Match 49.98; Score 1056; DB 9; Length 316;  
Best Local Similarity 54.48; Pred. No. 8.4e-53;  
Matches 234; Conservative 25; Mismatches 41; Indels 130; Gaps 8;  
QY 1 MGHHHHH---IEGR-----LKLDDNDVST--FSKLRLQGLPVTFQFDNL 44  
DB 1 MGSHHHHHSGISQGRSPCTEPTQPKKIVNAKDVNTKMFELKSR-----DTL 52  
QY 45 EKETGLRQEMSKDLEEVKAKVQPYLDDFOKKWQEMELYRQKVEPLRAELQEGAROKLH 104  
DB 53 AQEALLKEQALQTVSLKGSDEPP-----QSPW----- 81  
QY 105 ELQEKLSPLGEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARGARLAHYHAK 164  
DB 82 -----DRVKDLATVYD-----VLKDSGRDYVSQFEGS 109  
QY 165 ATEHLSTSEKAKPALEDLROGLLPVLESFKVSFLSALAEYTKKLTQGTCLKLDNDVSV 224  
DB 110 A-----LQKLNKLLDNDVSV 126  
QY 225 TSFSLRQGLPVTFQFDNLQETGLRQEMSKDLEEVKAKVQPYLDDFOKKWQEMELYRQKVE 284  
DB 127 TSFSLRQGLPVTFQFDNLQETGLRQEMSKDLEEVKAKVQPYLDDFOKKWQEMELYRQKVE 186  
QY 285 LYRQKVEPLRAELQEGAROKLHELOEKLSPLGEMDRARAHVDALRTHLAPYSDELQRL 344  
DB 187 LYRQKVEPLRAELQEGAROKLHELOEKLSPLGEMDRARAHVDALRTHLAPYSDELQRL 246  
QY 345 LAARLEALKENGARGARLAHYHAKATEHLSTSEKAKPALEDLROGLLPVLESFKVSFLSAL 404  
DB 247 LAARLEALKENGARGARLAHYHAKATEHLSTSEKAKPALEDLROGLLPVLESFKVSFLSAL 306  
QY 405 EYTKKLTQ 414  
DB 307 EYTKKLTQ 316

## RESULT 5

US-09-987-107-64  
; Sequence 64, Application US/09987107  
; Patent No. US20020156007A1  
; GENERAL INFORMATION:  
; APPLICANT: GRAVERSEN, Jonas  
; APPLICANT: MOESTRUP, Soren  
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES  
; FILE REFERENCE: GRAVERSENIA

; CURRENT APPLICATION NUMBER: US/09/987,107  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/264,022  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: DK PA2001 00057  
; PRIOR FILING DATE: 2001-01-15  
; PRIOR APPLICATION NUMBER: DK PA2000 01682  
; PRIOR FILING DATE: 2000-11-10  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 64  
; LENGTH: 324  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pT7H6 Trip-A-Tn-Apo A1-final - AmpR plasmid  
US-09-987-107-64  
Query Match 49.98; Score 1056; DB 9; Length 324;  
Best Local Similarity 56.3%; Pred. No. 8.6e-53;  
Matches 238; Conservative 32; Mismatches 45; Indels 108; Gaps 11;  
QY 1 MGHHHHH-----TEGRKLKLLDNDVSTSTFSKLRLQGLPVTFQFDNLQETGLRQ 53  
DB 1 MGSHHHHHSGISQGRSPGTE-----PPTQK-----PKKIVNAKK 38  
QY 54 EM--SKDLEEVKAKVQPYLDDFOKKWQEMELYRQKVEPLRAELQEGAROKLHELOEKLS 111  
DB 39 DVVNTKMFELKSR-----LDTL-----AQEALLKEQ-QALQTVSLKGT--KVIMKEPPQS 87  
QY 112 PLGEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARGARLAHYHAKATEHLST 171  
DB 88 P-WDRVKDLATVYD-----VLKDSGRDYVSQFEGSA----- 118  
QY 172 LSEKAKPALEDLROGLLPVLESFKVSFLSALAEYTKKLTQGTCLKLDNDVSTSTFSKL 231  
DB 119 -----LQKLNKLLDNDVSTSTFSKL 141  
QY 232 RQGLPVTFQFDNLQETGLRQEMSKDLEEVKAKVQPYLDDFOKKWQEMELYRQKVE 291  
DB 142 RQGLPVTFQFDNLQETGLRQEMSKDLEEVKAKVQPYLDDFOKKWQEMELYRQKVE 201  
QY 292 PLRAELOEGAROKLHELOEKLSPLGEMDRARAHVDALRTHLAPYSDELQRLAARLEA 351  
DB 202 PLRAELOEGAROKLHELOEKLSPLGEMDRARAHVDALRTHLAPYSDELQRLAARLEA 261  
QY 352 LKENGARGARLAHYHAKATEHLSTSEKAKPALEDLROGLLPVLESFKVSFLSALAEYTKKL 411  
DB 262 LKENGARGARLAHYHAKATEHLSTSEKAKPALEDLROGLLPVLESFKVSFLSALAEYTKKL 321  
QY 412 NTQ 414  
DB 322 NTQ 324  
RESULT 6  
US-09-987-107-54  
; Sequence 54, Application US/09987107  
; Patent No. US20020156007A1  
; GENERAL INFORMATION:  
; APPLICANT: GRAVERSEN, Jonas  
; APPLICANT: MOESTRUP, Soren  
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES  
; FILE REFERENCE: GRAVERSENIA  
; CURRENT APPLICATION NUMBER: US/09/987,107  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/264,022  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: DK PA2001 00057  
; PRIOR FILING DATE: 2001-01-15  
; PRIOR APPLICATION NUMBER: DK PA2000 01682  
; PRIOR FILING DATE: 2000-11-10  
; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 54  
; LENGTH: 316  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pT7H6 Trip-A-Apo A1 K9A K15A - AmpR plasmid  
US-09-987-107-54

Query Match 49.6%; Score 1051; DB 9; Length 316;  
Best Local Similarity 54.9%; Pred. No. 1.6e-52;  
Matches 236; Conservative 22; Mismatches 42; Indels 130; Gaps 9;  
QY 1 MGHHHHHH-----IEGR-----KLLDN--WDSV--TSTFSKLEQLGPTVQTEFWNDL 44  
DB 1 MGSHHHHHSGISQGRSGTEPTQPKAIVNAKADVVNTKMFELKSR-----DTL 52  
QY 45 EKETGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLH 104  
DB 53 AQEALLKEQALQTVSLKGSDEPP-----QSPW----- 81  
QY 105 ELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAK 164  
DB 82 -----DRVKDLATVYD-----VLDKSGROYVSQFEGS 109  
QY 165 ATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEYTKLNTQGTFLKLLDNWDSV 224  
DB 110 A-----LGKQLNLKLLDNWDSV 126  
QY 225 TSTFSKLEQLGPTVQTEFWNDLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEME 284  
DB 127 TSTFSKLEQLGPTVQTEFWNDLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEME 186  
QY 285 LYRQKVEPLRAELQEGARQKLHELOEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQ 344  
DB 187 LYRQKVEPLRAELQEGARQKLHELOEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQ 246  
QY 345 LAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSAL 404  
DB 247 LAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSAL 306  
QY 405 EYTKKLLNTQ 414  
DB 307 EYTKKLLNTQ 316

RESULT 7  
US-09-987-107-66  
; Sequence 66, Application US/09987107  
; Patent No. US20020156007A1  
; GENERAL INFORMATION:  
; APPLICANT: GRAVERSEN, Jonas  
; APPLICANT: MOESTRUP, Soren  
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES  
; FILE REFERENCE: GRAVERSENIA  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR FILING DATE: 2001-01-15  
; PRIOR FILING DATE: 2000-11-10  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 66  
; LENGTH: 324  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pT7H6 Trip-A-Tn-Apo A1 final K9AK15A - AmpR plasmid  
US-09-987-107-66

Query Match 49.6%; Score 1051; DB 9; Length 324;  
Best Local Similarity 56.3%; Pred. No. 1.7e-52;  
Matches 238; Conservative 30; Mismatches 47; Indels 108; Gaps 11;  
QY 1 MGHHHHHH-----IEGRKLLDNWDSVTSTFSKLEQLGPTVQTEFWNDLEKETEGRLQ 53  
DB 1 MGSHHHHHSGISQGRSGTE-----PPTQK-----PKAIVNAKA 38  
QY 54 EM--SKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLS 111  
DB 39 DVVNTKMFEEELKSR-----LDTL-----AQEALLKEQ-QALQTVSLKGT--KVHMKPEPPQS 87  
QY 112 PLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLST 171  
DB 88 P-WDRVKDLATVYD-----VLDKSGRDIYSQFEGSA----- 118  
QY 172 LSEKAKPALEDLRQGLLPVLESFKVSFLSALEYTKLNTQGTFLKLLDNWDSVTSTFSKL 231  
DB 119 -----LGKQLNLKLLDNWDSVTSTFSKL 141  
QY 232 REQLGPTVQTEFWNDLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVE 291  
DB 142 REQLGPTVQTEFWNDLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVE 201  
QY 292 PLRAELQEGARQKLHELOEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEA 351  
DB 202 PLRAELQEGARQKLHELOEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEA 261  
QY 352 LKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEYTKKL 411  
DB 262 LKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEYTKKL 321  
QY 412 NTQ 414  
DB 322 NTQ 324

RESULT 8  
US-09-987-107-58  
; Sequence 58, Application US/09987107  
; Patent No. US20020156007A1  
; GENERAL INFORMATION:  
; APPLICANT: GRAVERSEN, Jonas  
; APPLICANT: MOESTRUP, Soren  
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES  
; FILE REFERENCE: GRAVERSENIA  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR FILING DATE: 2001-01-15  
; PRIOR FILING DATE: 2000-11-10  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 58  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pT7H6 Trip-A-Fn-Apo A1-final - AmpR plasmid  
US-09-987-107-58

Query Match 49.6%; Score 1049.5; DB 9; Length 323;  
Best Local Similarity 56.4%; Pred. No. 2e-52;  
Matches 235; Conservative 24; Mismatches 61; Indels 97; Gaps 8;  
QY 1 MG-HHHHHHIEGRKLLDNWDSVTSTFSKLEQLGPTVQTEFWNDLEKETEGRLQEMSKDL 59  
DB 1 MGSHHHHHSGIS-----GSTQGRSPGTEPTQPK 31  
QY 60 EEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLGEEMRD 119

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Db 32 KIVNAK-----KSRDLTL---AQEVALLKEQQAQTIVSLKGTSGQD 81
QY 120 RARAHVDALRTHLAPYS--DELQRRLAARLEALKENGARGARLAAYHAKATEHLSTLSEKAK 177
Db 82 E-----PPQSPWDRVKDLATVYVDVKDSGRDYVSQFEGSA----- 117
QY 178 PALEDLRQGLLPVLESFKVSLSALEEYTKKLTNTOGTLKLLDNWDSVTSTFSKLRQGLGP 237
Db 118 -----LGRQLNKLKLLDNWDSVTSTFSKLRQGLGP 146
QY 238 VTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDPFQKKWQEMELYRQKVPEPLRAEL 297
Db 147 VTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDPFQKKWQEMELYRQKVPEPLRAEL 206
QY 298 QEGARQKHLHELOEKLSPGLGEEMDRARAHVDALRTHLAPYSDELQRRLAARLEALKENG 357
Db 207 QEGARQKHLHELOEKLSPGLGEEMDRARAHVDALRTHLAPYSDELQRRLAARLEALKENG 266
QY 358 ARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSLSALEEYTKKLTNTQ 414
Db 267 ARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSLSALEEYTKKLTNTQ 323

RESULT 9
US-09-987-107-56
; Sequence 56, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p7H6 Trip-A-Fn-Apo A1 - AmpR plasmid
US-09-987-107-56

Query Match 49.5%; Score 1047.5; DB 9; Length 323;
Best Local Similarity 56.4%; Pred. No. 2.6e-52;
Matches 235; Conservative 23; Mismatches 62; Indels 97; Gaps 8;

QY 1 MG-HHHHHHTEGRLKLLDNWDSVTSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDL 59
Db 1 MGSHHHHHHSGS-----GSIQGRSPGTEPPTQPKP 31

QY 60 EEVKAQVQPYLDDPFQKKWQEMELYRQKVPEPLRAELQEGARQKHLHELOEKLSPGLGEEMDR 119
Db 32 KIVNAK-----KDVNTKMEEL---KSRDLTL---AQEVALLKEQQAQTIVSLKGTSGQD 81
QY 120 RARAHVDALRTHLAPYS--DELQRRLAARLEALKENGARGARLAAYHAKATEHLSTLSEKAK 177
Db 82 E-----PPQSPWDRVKDLATVYVDVKDSGRDYVSQFEGSA----- 117
QY 178 PALEDLRQGLLPVLESFKVSLSALEEYTKKLTNTOGTLKLLDNWDSVTSTFSKLRQGLGP 237
Db 118 -----LGRQLNKLKLLDNWDSVTSTFSKLRQGLGP 146
QY 238 VTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDPFQKKWQEMELYRQKVPEPLRAEL 297
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Db 147 VTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDPFQKKWQEMELYRQKVPEPLRAEL 206
QY 298 QEGARQKHLHELOEKLSPGLGEEMDRARAHVDALRTHLAPYSDELQRRLAARLEALKENG 357
Db 207 QEGARQKHLHELOEKLSPGLGEEMDRARAHVDALRTHLAPYSDELQRRLAARLEALKENG 266
QY 358 ARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSLSALEEYTKKLTNTQ 414
Db 267 ARLAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSLSALEEYTKKLTNTQ 323

RESULT 10
US-09-987-107-60
; Sequence 60, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p7H6 Trip-A-Fn-Apo A1 final K9AK15A - AmpR plasmid
US-09-987-107-60

Query Match 49.4%; Score 1045.5; DB 9; Length 323;
Best Local Similarity 72.9%; Pred. No. 3.4e-52;
Matches 226; Conservative 19; Mismatches 53; Indels 12; Gaps 4;

QY 111 SPLGEEMDRARAHVDALRTHLAPYSDELQRRLAARLEALKENGARGARLAAYHAKATEHLS 170
Db 20 SPGTEPTQPKAIVNAKADVV---NTKMFEEKSRDLTLAQE-VALLKEQQAQTIVSLK 75
QY 171 TLSEKAKP-----ALEDLRQGLLPVLESFKVSLSALEEYTKKLTNTOGTLKLLDNWDSV 224
Db 76 GTSQDEPPQSPWDRVKDLATVYVDVKDSGRDYVSQFE--GSALGKQLNKLKLLDNWDSV 133
QY 225 TSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDPFQKKWQEME 284
Db 134 TSTFSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDPFQKKWQEME 193
QY 285 LYRQKVPEPLRAELQEGARQKHLHELOEKLSPGLGEEMDRARAHVDALRTHLAPYSDELQR 344
Db 194 LYRQKVPEPLRAELQEGARQKHLHELOEKLSPGLGEEMDRARAHVDALRTHLAPYSDELQR 253
QY 345 LAARLEALKENGARGARLAAYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVSLSA 404
Db 254 LAARLEALKENGARGARLAAYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVSLSA 313
QY 405 EYTKKLTNTQ 414
Db 314 EYTKKLTNTQ 323

RESULT 11
US-09-987-107-8
; Sequence 8, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
```

Query Match 49.28; Score 1042; DB 9; Length 304;  
Best Local Similarity 72.98; Pred. No. 5e-52;  
Matches 226; Conservative 19; Mismatches 53; Indels 12; Gaps 4;

Qy	111	SPLGEEMDRARAHVDALRTHLAPYSDELQRRLAARLEALKENGARLAEYHAKATEHLS	170
Db	1	SGTEPTPTQKPAIYNKADVV---NTKMFEELKSRDLTLAQE-VALLKEQQAQTVSLSK	56
Qy	171	TJSEKAKP-----ALEDLROGLLPVLSEFKVSPFLSALEYTKLNTQGTILKLDNWDVS	224
Db	57	GTSGQDEPPQSPWDRVKDLATVYVDVLKDSGRDVSQFE--GSALGKQLNLKLDNWDVS	114
Qy	225	TSTFSKLRQLGPGVTQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDDFQKKQOEEME	284
Db	115	TSTFSKLRQLGPGVTQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDDFQKKQOEEME	174
Qy	285	LYRQKVEPLRAELQEGARQKLHELQEKLSPLGSEMRDRARAHVDALRTHLAPYSDELQR	344
Db	175	LYRQKVEPLRAELQEGARQKLHELQEKLSPLGSEMRDRARAHVDALRTHLAPYSDELQR	234
Qy	345	LAARLEALKENGARLAEYHAKATEHLSLTSEKAKPALEDLROGLLPVLSEFKVSPFLSA	404
Db	235	LAARLEALKENGARLAEYHAKATEHLSLTSEKAKPALEDLROGLLPVLSEFKVSPFLSA	294
Qy	405	EYTKKLNLTQ 414	
Db	295	EYTKKLNLTQ 304	

RESULT 12  
US-09-987-107-7  
; Sequence 7, Application US/09987107  
; Patent No. US20020156007A1  
; GENERAL INFORMATION:  
; APPLICANT: GRAVERSEN, Jonas  
; APPLICANT: MOESTRUP, Soren  
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES  
; FILE REFERENCE: GRAVERSENIA  
; CURRENT APPLICATION NUMBER: US/09/987.107  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/264,022



```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7 H6 Fx Cys-Apo A1 plasmid
US-09-987-107-52

Query Match      49.1%; Score 1039.5; DB 9; Length 261;
Best Local Similarity 80.8%; Pred. No. 5.9e-52;
Matches 211; Conservative 0; Mismatches 1; Indels 49; Gaps 2;

QY 1 MGHHHHH---TEGR-----12
Db 1 MGHHHHHHSGTEGRGDDPPQSPWDRVKDLATYVVDVKDSGRDYVSQFEGSALGKQL 60

QY 13 -LKLLDNWDSVSTFSKLRQGLPGVPTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLD 71
Db 61 NLKLLDNWDSVSTFSKLRQGLPGVPTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLD 120

QY 72 DFQKKQWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMDRARAHVDALRTH 131
Db 121 DFQKKQWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMDRARAHVDALRTH 180

QY 132 LAPYSDLRQRLAARLEALKENGARLAIEYHAKATEHLSLSEKAKPALEDLRQGLLPVL 191
Db 181 LAPYSDLRQRLAARLEALKENGARLAIEYHAKATEHLSLSEKAKPALEDLRQGLLPVL 240

QY 192 ESFKVSFSLSEAEYTKKLNQ 212
Db 241 ESFKVSFSLSEAEYTKKLNQ 261

RESULT 14
US-09-987-107-6
; Sequence 6, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(58)
; OTHER INFORMATION: Trimerisation module from tetranectin
; NAME/KEY: misc_feature
; LOCATION: (59)..(61)
; OTHER INFORMATION: Linker
; NAME/KEY: misc_feature
; LOCATION: (62)..(304)
; OTHER INFORMATION: Mature Apo A1
US-09-987-107-6

Query Match      49.08%; Score 1038; DB 9; Length 304;
Best Local Similarity 72.5%; Pred. No. 8.3e-52;
Matches 224; Conservative 17; Mismatches 52; Indels 16; Gaps 4;

QY 112 PLGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAIEYHAKATEHLS 171
Db 6 PPTQPKRIVNAKDVNT-----KMFELKSRDLTLAGQ-VALLKEQALQTVSLKG 57

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7 H6 Fx Cys-Apo A1 plasmid
US-09-987-107-52

Query Match      48.9%; Score 1036.5; DB 9; Length 301;
Best Local Similarity 73.3%; Pred. No. 1e-51;
Matches 225; Conservative 18; Mismatches 55; Indels 9; Gaps 4;

QY 111 SPLGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAIEYHAKATEHLS 170
Db 1 SPQTEPTQPKRAIVNAKADV---NTKMFELKSRDLTLAGQ-VALLKEQALQTVSLK 56

QY 171 TLSEKAK---PALEDLRQGLLPVLESFKVSFSLSEAEYTKKLNQGTKLKLLDNWDSVT 227
Db 57 GSDEPPQSPWDRVKDLATYVVDVKDSGRDYVSQFEGSALGKQLNKLKLLDNWDSVT 114

QY 228 FSKLRQGLPGVPTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKQWQEMEL 287
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Db	115	FSKLREQLPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKWQEMELYR	174
Qy	288	QKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDELQRORLAA	347
Db	175	QKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDELQRORLAA	234
Qy	348	RLEALKENGARLAAYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVSFSLALEEY	407
Db	235	RLEALKENGARLAAYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVSFSLALEEY	294
Qy	408	TKKLNTQ	414
Db	295	TKKLNTQ	301

Search completed: April 30, 2003, 15:19:27  
Job time : 48 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 30, 2003, 15:10:37 ; Search time 22 Seconds  
(without alignments)  
1809.075 Million cell updates/sec

Title: US-09-990-087-17  
Perfect score: 2118  
Sequence: 1 MGHHHHHIEGRLLKLLDND.....SFKVSFLSALEETKLLNTQ 414

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1024	48.3	267	1 LPHUA1	apolipoprotein A-I
2	991.5	46.8	267	1 A26529	apolipoprotein A-I
3	991.5	46.8	267	2 JS0079	apolipoprotein A-I
4	860.5	40.6	266	1 LPDGA1	apolipoprotein A-I
5	837	39.5	266	1 LPRB1Z	apolipoprotein A-I
6	825.5	39.0	241	2 A24998	apolipoprotein A-I
7	818.5	38.6	265	1 LPRB1B	apolipoprotein A-I
8	809	38.2	265	2 A46018	apolipoprotein A-I
9	809	38.2	265	2 JT0672	apolipoprotein A-I
10	803	37.9	265	2 A56858	apolipoprotein A-I
11	796.5	37.6	264	2 S31394	apolipoprotein A-I
12	789.5	37.3	231	2 JQ0704	apolipoprotein A-I
13	653	30.8	284	2 S22420	apolipoprotein A-I
14	647	30.5	262	2 J21237	apolipoprotein A-I
15	617.5	29.2	164	2 S21830	apolipoprotein A-I
16	591	27.9	259	2 A24700	apolipoprotein A-I
17	505.5	23.9	246	2 A61448	apolipoprotein A-I
18	491.5	23.2	264	1 LPCHA1	apolipoprotein A-I
19	470.5	22.2	264	2 JC3456	apolipoprotein A-I
20	350.5	16.5	429	2 S29565	apolipoprotein A-I
21	339.5	16.0	401	2 A47141	apolipoprotein A-I
22	324.5	15.3	396	1 LPHUA4	apolipoprotein A-I
23	291.5	13.8	391	1 LPRTA4	apolipoprotein A-I
24	283	13.4	399	2 C40892	apolipoprotein A-I
25	279	13.2	391	2 B40892	apolipoprotein A-I
26	279	13.2	395	2 A40892	apolipoprotein A-I
27	275	13.0	394	2 A25281	apolipoprotein A-I
28	251	11.9	1547	2 T28657	blackjack protein,
29	222	10.5	1938	2 JC5421	smooth muscle myos

30	222	10.5	1972	2 JC5420	smooth muscle myos
31	219.5	10.4	1410	1 A57013	early endosome ant
32	216.5	10.2	1039	2 S18199	myosin heavy chain
33	214	10.1	3187	2 JC5837	364K Golgi Complex
34	209.5	9.9	1979	1 S03166	myosin heavy chain
35	209	9.9	1999	1 S21801	myosin heavy chain
36	208.5	9.8	1934	2 I48153	myosin heavy chain
37	208	9.8	880	2 F75103	conserved hypotet
38	208	9.8	886	2 H69378	conserved hypotet
39	208	9.8	978	2 A70387	conserved hypotet
40	207.5	9.8	1938	2 A59293	skeletal myosin he
41	207	9.8	1972	1 A41604	myosin heavy chain
42	205.5	9.7	1935	2 A5286	myosin heavy chain
43	205.5	9.7	2007	1 B43402	myosin heavy chain
44	205	9.7	1935	1 A37102	myosin beta heavy
45	204.5	9.7	1938	1 A40997	myosin heavy chain

ALIGNMENTS

RESULT 1

LPHUA1

apolipoprotein A-I precursor [validated] - human

N:Alternate names: apoA-I-2; apoA-I-4; preproapoA-I; prostacyclin stabilizing factor

C:Species: Homo sapiens (man)

C>Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 08-Dec-2000

C:Accession: A90947; B90947; S02373; A93465; A21147; A93519; B93519; A93472; A94010; 6197

R:Seilhamer, J.J.; Protter, A.A.; Frossard, P.; Levy-Wilson, B.

DNA 3, 309-317, 1984

A:Title: Isolation and DNA sequence of full-length cDNA and of the entire gene for hu

A:Reference number: A90947; MUID:85026665; PMID:6207999

A:Accession: A90947

A:Molecule type: DNA

A:Residues: 1-267 <SEI>

A:Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635

A:Accession: B90947

A:Molecule type: mRNA

A:Residues: 1-267 <SE2>

A:Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635

R:Makrides, S.C.; Ruiz-Opazo, N.; Hayden, M.; Nussbaum, A.L.; Breslow, J.L.; Zannis, Eur. J. Biochem. 173, 465-471, 1988

A:Title: Sequence and expression of Tangier apoA-I gene.

A:Reference number: S02373; MUID:86196137; PMID:3129297

A:Accession: S02373

A:Molecule type: DNA

A:Residues: 1-267 <MAK>

A:Cross-references: EMBL:X07496; NID:g28774; PIDN:CAA30377.1; PID:g296729

R:Shoulders, C.C.; Kornblitt, A.R.; Munro, B.S.; Baralle, F.E.

Nucleic Acids Res. 11, 2827-2837, 1983

A:Title: Gene structure of human apolipoprotein AI.

A:Reference number: A93465; MUID:83220822; PMID:6406984

A:Accession: A93465

A:Molecule type: DNA

A:Residues: 1-267 <SHO>

A:Cross-references: GB:J00098; GB:J00100; GB:J00101; GB:J03222; GB:K01518;

R:Karathanasis, S.K.; Zannis, V.I.; Breslow, J.L.

Proc. Natl. Acad. Sci. U.S.A. 80, 6147-6151, 1983

A:Title: Isolation and characterization of the human apolipoprotein A-I gene.

A:Reference number: A21147; MUID:84016011; PMID:6413973

A:Accession: A21147

A:Molecule type: DNA

A:Residues: 1-267 <KAR>

A:Cross-references: GB:J00098; GB:J03222; NID:g178765; PIDN:AAB59514.1; PID:g178768

R:Sharpe, C.R.; Stodli, A.; Shelley, C.S.; Lucero, M.A.; Shoulders, C.C.; Baralle, F.

Nucleic Acids Res. 12, 3917-3932, 1984

A:Title: Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA abundan

A:Reference number: A93519; MUID:84221405; PMID:6328445

A:Accession: A93519

A:Molecule type: mRNA

A:Residues: 1-267 <SHQ>

A:Cross-references: GB:X00566; NID:g28765; PIDN:CAA25232.1; PID:g732753

A:Accession: B93519  
A:Molecule type: DNA  
A:Residues: 1-24 <SH2>  
R:Cheung, P.; Chan, L.  
Nucleic Acids Res. 11, 3703-3715, 1983  
A:Title: Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.  
A:Reference number: A93472; MUID:83220772; PMID:6304641  
A:Accession: A93472  
A:Molecule type: mRNA  
A:Residues: 1-267 <CHE>  
A:Cross-references: GB:J000098; GB:J000099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GB:R:Law, S.W.; Brewer Jr., H.B.  
Proc. Natl. Acad. Sci. U.S.A. 81, 66-70, 1984  
A:Title: Nucleotide sequence and the encoded amino acids of human apolipoprotein A-I mRNA  
A:Reference number: A94010; MUID:84119464; PMID:6198645  
A:Accession: A94010  
A:Molecule type: mRNA  
A:Residues: 1-267 <LAW>  
A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GB:R:Zannis, V.I.; Karathanasis, S.K.; Keutmann, H.T.; Goldberger, G.; Breslow, J.L.  
Proc. Natl. Acad. Sci. U.S.A. 80, 2574-2578, 1983  
A:Title: Intracellular and extracellular processing of human apolipoprotein A-I: secreted  
A:Reference number: A21118; MUID:83195100; PMID:6405383  
A:Accession: A21118  
A:Molecule type: mRNA  
A:Residues: 1-24 <ZAN>  
R:Brewer Jr., H.B.; Fairwell, T.; Kay, L.; Meng, M.; Ronan, R.; Law, S.; Light, J.A.  
Biochem. Biophys. Res. Commun. 113, 626-632, 1983  
A:Title: Human plasma preapoA-I: isolation and amino-terminal sequence.  
A:Reference number: A90112; MUID:83256553; PMID:6409108  
A:Accession: A90112  
A:Molecule type: protein  
A:Residues: 19-27 <BRE>  
R:Brewer Jr., H.B.; Fairwell, T.; LaRue, A.; Ronan, R.; Houser, A.; Bronzert, T.J.  
Biochem. Biophys. Res. Commun. 80, 623-630, 1978  
A:Title: The amino acid sequence of human APOA-I, an apolipoprotein isolated from high density lipoproteins.  
A:Reference number: A90209; MUID:78123731; PMID:204308  
A:Accession: A90209  
A:Molecule type: protein  
A:Residues: 25-57, 'O', 59-169, 'QQ', 172-267 <BR2>  
R:Yui, Y.; Aoyama, T.; Morishita, H.; Takahashi, M.; Takatsu, Y.; Kawai, C.  
J. Clin. Invest. 82, 803-807, 1988  
A:Title: Serum prostacyclin stabilizing factor is identical to apolipoprotein A-I (Apo A-I).  
A:Reference number: A30516; MUID:88331387; PMID:3047170  
A:Accession: A30516  
A:Molecule type: protein  
A:Residues: 25-56 <YUI>  
R:Nichols, W.C.; Dwulet, F.E.; Liepnieks, J.; Benson, M.D.  
Biochem. Biophys. Res. Commun. 156, 762-768, 1988  
A:Title: Variant apolipoprotein AI as a major constituent of a human hereditary amyloid.  
A:Reference number: A31582; MUID:89050104; PMID:3142462  
A:Accession: A31582  
A:Molecule type: protein  
A:Residues: 25-49, 'R', 51-85, 'D', 87-107 <NIC>  
A:Note: variant sequence from patient with familial amyloidotic polyneuropathy type III  
R:Manjunath, P.; Marcel, Y.L.; Uma, J.; Seidah, N.G.; Chretien, M.; Chapdelaine, A.  
J. Biol. Chem. 264, 16853-16857, 1989  
A:Title: Apolipoprotein A-I binds to a family of bovine seminal plasma proteins.  
A:Reference number: A34409; MUID:89380318; PMID:2506184  
A:Accession: A34409  
A:Molecule type: protein  
A:Residues: 25-48 <MAN>  
R:Stoffel, W.; Binczek, E.  
Biol. Chem. Hoppe-Seyler 369, 1055-1063, 1988  
A:Title: Structural requirements of human preapoApolipoprotein AI for translocation and  
A:Reference number: S02737; MUID:89149957; PMID:3228490  
A:Accession: S02737  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-6, 'AV', 9, 'LV', 12-29 <STO>  
A:Note: part of this sequence, including the amino end of the mature protein, was confirmed  
R:Stoffel, W.; Binczek, E.  
Biol. Chem. Hoppe-Seyler 372, 481-488, 1991

A:Title: Transient expression of wild type and mutant human apolipoprotein AI in COS  
A:Reference number: S16197; MUID:92029676; PMID:1930731  
A:Contents: annotation; extension of studies in reference S02737  
R:Stoffel, W.; Kruger, E.; Deutzmann, R.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 227-237, 1983  
A:Title: Cell-free translation of human liver apolipoprotein AI and AII mRNA processes  
A:Reference number: A19913; MUID:83236195; PMID:6407957  
A:Accession: B19913  
A:Molecule type: protein  
A:Residues: 1-6, 'X', 8-13, 'XXX', 17-18, 'XX', 21, 'X', 23-25, 'X', 27-29 <ST2>  
R:Ehnholm, C.; Boras, S.E.; Tenkanen, H.; Kirszbaum, L.; Metsä, J.; Murphy, B.; Walke  
Biochim. Biophys. Acta 1086, 255-260, 1991  
A:Title: The apolipoprotein A-I binding protein of placenta and the SP-40.40 protein  
A:Reference number: A56815; MUID:92075698; PMID:1742316  
A:Accession: A56815  
A:Molecule type: protein  
A:Residues: 25-31, 'P', 33 <EHN>  
A:Experimental source: Serum  
A:Note: sequence extracted from NCBI backbone (NCBIP:69759)  
A:Note: 32-Tip was also found  
R:Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.  
Biochemistry 33, 1988-1993, 1994  
A:Title: Identification of proteins associated with apolipoprotein A-I-containing lip  
A:Reference number: A54223; MUID:94162201; PMID:8117655  
A:Accession: A54223  
A:Molecule type: protein  
A:Residues: 25-39 <KUN>  
R:Mogulievsky, N.; Roobol, C.; Loriau, R.; Guillaume, J.P.; Jacobs, P.; Cravador, A.;  
DNA 8, 429-436, 1989  
A:Title: Production of human recombinant proapolipoprotein A-I in *Escherichia coli*: p  
A:Reference number: I39476; MUID:89377481; PMID:2673706  
A:Accession: I39476  
A:Molecule type: mRNA  
A:Residues: 19-267 <RES>  
A:Cross-references: GB:M25068; NID:gl78774; PIDN:AAA51747.1; PID:gl78775  
R:Higuchi, K.; Law, S.W.; Hoeg, J.M.; Schumacher, U.K.; Meglin, N.; Brewer, H.B.  
J. Biol. Chem. 263, 18530-18536, 1988  
A:Title: Tissue-specific expression of apolipoprotein A-I (ApoA-I) is regulated by th  
A:Reference number: I39475; MUID:89054040; PMID:3142880  
A:Accession: I39475  
A:Molecule type: DNA  
A:Residues: 1-14 <RE2>  
A:Cross-references: GB:J04066; NID:gl78763; PIDN:AAA51746.1; PID:g553183  
R:Breslow, J.L.  
Annu. Rev. Biochem. 54, 699-727, 1985  
A:Title: Human apolipoprotein molecular biology and genetic variation.  
A:Reference number: A90042; MUID:85278004; PMID:3896129  
A:Contents: annotation; review of sequences, variants and gene location  
R:Hoeg, J.M.; Meng, M.S.; Ronan, R.; Fairwell, T.; Brewer Jr., H.B.  
J. Biol. Chem. 261, 3911-3914, 1986  
A:Title: Human apolipoprotein A-I. Post-translational modification by fatty acid acyl  
A:Reference number: A92577; MUID:86140194; PMID:3005308  
A:Contents: annotation; acylation with palmitate  
A:Note: an undetermined serine or threonine is acylated by fatty acid; the acylating  
R:Law, S.W.; Brewer, H.B.  
J. Biol. Chem. 260, 12810-12814, 1985  
A:Title: Tangier disease: The complete mRNA sequence encoding for preapoA-A-I.  
A:Reference number: I55236; MUID:86008382; PMID:2995392  
A:Accession: I55236  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-143, 'D', 145-267 <RE3>  
A:Cross-references: GB:M11791; NID:gl78776; PIDN:AAA35545.1; PID:gl78777  
C:Comment: Apolipoprotein A-I precursor is synthesized in the liver and small intestine  
A:Protein (HDL) in plasma.  
C:Genetics:  
A:Gene: GDB:APOA1  
A:Cross-references: GDB:119684; OMIM:107680  
A:Map position: 11q23.3-11q23.3  
A:Introns: 15/1; 67/2  
C:Function:  
A:Description: participates in the reverse transport of cholesterol from tissues to t  
sterol acyltransferase (LCAT); noncovalently binds and stabilizes prostacyclin (PGI-2



|||||  
Db 230 KAKPALEDLROGLLPVLESEFKVSLSALEYTKKLSQ 267

## RESULT 4

LPDGA1

apolipoprotein A-I precursor - dog

C:Species: Canis lupus familiaris (dog)

C:Date: 17-Dec-1982 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999

C:Accession: A60940; A03092; A61418

R:Luo, C.C.; Li, W.H.; Chan, L.

J. Lipid Res. 30, 1735-1746, 1989

A:Title: Structure and expression of dog apolipoprotein A-I, E, and C-I mRNAs: implications

A:Reference number: A60940; MUID:90132271; PMID:2515239

A:Accession: A60940

A:Molecule type: mRNA

A:Residues: 1-266 &lt;LUD&gt;

R:Chung, H.; Randolph, A.; Reardon, I.; Heinrikson, R.L.

J. Biol. Chem. 257, 2961-2967, 1982

A:Title: The covalent structure of apolipoprotein A-I from canine high density lipoproteins

A:Reference number: A03092; MUID:82142425; PMID:6801039

A:Accession: A03092

A:Molecule type: protein

A:Residues: 25-167, 'G', 169-201, 'Q', 203-234, 'Q', 236-266 &lt;CHU&gt;

R:Nakai, T.; Wayne, T.F.; Tang, J.

FEBS Lett. 64, 409-411, 1976

A:Title: The amino- and carboxyl-terminal sequences of canine apolipoprotein A-I.

A:Reference number: A61418; MUID:76210910; PMID:179887

A:Accession: A61418

A:Molecule type: protein

A:Residues: 25-56, 'Z', 261-262, 'A' &lt;NAK&gt;

C:Superfamily: apolipoprotein A-I

C:Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid transport; lipoprotein

F:1-18/Domain: signal sequence #status predicted &lt;SIG&gt;

F:19-24/Domain: propeptide #status predicted &lt;PRO&gt;

F:25-266/Product: apolipoprotein A-I #status experimental &lt;MAT&gt;

Query Match 40.6%; Score 860.5; DB 1; Length 266;

Best Local Similarity 62.9%; Pred. No. 1.9e-33;

Matches 175; Conservative 26; Mismatches 34; Indels 43; Gaps 1;

QY 137 DELRQRLAARLEALKENGARLAAYHAKATEHLSLSEKAKPALEDLROGLLPVLESEFKV 196

Db 32 DRVKDLATVYDVAVKDSGRDYVAQFEASA----- 60

QY 197 SPLSALEYTKKLNQGTGLKLLDNWDSVTSTFSKLREQLGPTQEFWDLNLEKETGLRQE 256

Db 61 -----LGQQLNKLKLLDNWDSLSSTVTKLREQIGPTQEFWDLNLEKETGLRQE 108

QY 257 MSKDLEEVKAVQPYLDLDFQKKQWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLG 316

Db 109 MSKDLEEVKAVQPYLDLDFQKKQWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLA 168

QY 317 EEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSLSE 376

Db 169 EELRDSARTHTVDTLRKLAPYSNELQRLAARLESIKEGGASLAAYQAKAREHLSVLS 228

QY 377 KAKPALEDLROGLLPVLESEFKVSLSALEYTKKLNQ 414

Db 229 KAKPALEDLROGLLPVLESEFKVSLSALEYTKKLNQ 266

RESULT 5

LPRB12

apolipoprotein A-I precursor (clone 22ap AI) - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 22-Jun-1999

C:Accession: S06064

R:Paraskovopoulou, T.B.; Kriti, A.; Zannis, V.

submitted to the EMBL Data Library, July 1989

A:Reference number: S06064

A:Accession: S06064

A:Molecule type: mRNA

A:Residues: 1-266 &lt;PAR&gt;

A:Cross-References: EMBL:X15908; NID:gl457; PIDN:CAA34024.1; PID:gl458

C:Comment: This protein is synthesized in the small intestine.

C:Comment: This protein is a major component of the high density lipoproteins in plas

C:Superfamily: apolipoprotein A-I

C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem r

F:1-18/Domain: signal sequence #status predicted &lt;SIG&gt;

F:19-24/Domain: propeptide #status predicted &lt;PRO&gt;

F:25-266/Product: apolipoprotein A-I #status experimental &lt;MAT&gt;

Query Match 39.5%; Score 837; DB 1; Length 266;

Best Local Similarity 61.2%; Pred. No. 2.3e-32;

Matches 170; Conservative 31; Mismatches 34; Indels 43; Gaps 2;

QY 137 DELRQRLAARLEALKENGARLAAYHAKATEHLSLSEKAKPALEDLROGLLPVLESEFKV 196

Db 32 DKIKDFATVYDVTKDSGREYVAQFEASA----- 60

QY 197 SPLSALEYTKKLNQGTGLKLLDNWDSVTSTFSKLREQLGPTQEFWDLNLEKETGLRQE 256

Db 61 -----FGQQLN-----LKLLDNWDSLSSTVSKLREQLGPTQEFWDLNLEKETGLRQE 108

QY 257 MSKDLEEVKAVQPYLDLDFQKKQWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLG 316

Db 109 MNKDLQEVKQVQPYLDFEQKKQWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLA 168

QY 317 EEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSLSE 376

Db 169 EELRDSARTHTVDTLRKLAPYSNELQRLAARLESIKEGGASLAAYQAKAREHLSVLS 228

QY 377 KAKPALEDLROGLLPVLESEFKVSLSALEYTKKLNQ 414

Db 229 KAKPALEDLROGLLPVLESEFKVSLSALEYTKKLNQ 266

RESULT 6

A24998

apolipoprotein A-I - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 31-Dec-1993

C:Accession: A24998

R:Yang, C.; Yang, T.; Pownall, H.J.; Gotto Jr., A.M.

Eur. J. Biochem. 160, 427-431, 1986

A:Title: The primary structure of apolipoprotein A-I from rabbit high-density lipopro

A:Reference number: A24998; MUID:87030294; PMID:3095115

A:Accession: A24998

A:Molecule type: protein

A:Residues: 1-241 &lt;YAN&gt;

C:Superfamily: apolipoprotein A-I

C:Keywords: HDL; lipid binding; lipoprotein

Query Match 39.0%; Score 825.5; DB 2; Length 241;

Best Local Similarity 58.4%; Pred. No. 7e-32;

Matches 173; Conservative 28; Mismatches 40; Indels 55; Gaps 3;

QY 119 DRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSLSEKAKP 178

Db 1 DEPRSDWKTKDFATVYD-----VKDSGREYVAQFEASA----- 35

QY 179 ALEDLROGLLPVLESEFKVSLSALEYTKKLNQGTGLKLLDNWDSVTSTFSKLREQLG 238

Db 36 -----FGQQLN-----LKLLDNWDSLSSTVSKLREQLG 65

QY 239 TQEFWDLNLEKETGLRQEMSKDLEEVKAVQPYLDLDFQKKQWQEMELYRQKVEPLRAELQ 298

Db 66 TQEFWDLNLEKETGLRQEMSKDLEEVKAVQPYLDLDFQKKQWQEMELYRQKVEPLRAELQ 125

QY 299 EGARQKLHELQEKLSPLGSEEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENG 358

Db 126 ESARQKLHELQEKLSPLAELRDSARTHTVDTLRKLAPYSQELQRLAARLESIKEGGA 185

QY 359 RLAEYHAKATEHLSLSEKAKPALEDLROGLLPVLESEFKVSLSALEYTKKLNQ 414



QY 197 SFLSALEEYTKKLTQGTFLKLLDNWDSVTSTFSKLRQGLGVPVTOEFWDNLEKETEGLRQE 256  
Db 59 ---SALGKHLK-----LKLNDWDSLGSTFTKVRQGLGVPVTOEFWDNLEKETEGLRQE 108  
QY 257 MSKDLSEEVKAKVQPYLDLDFQKQWQEMELYRQKVEPLRAELQEGARQKHLQEKLSPLG 316  
Db 109 MSKDLSEEVKAKVQPYLDLDFQKQWQEMELYRQKVEPLRAELQEGARQKHLQEKLSPLA 168  
QY 317 EEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKEKNGGARLAEYHAKATEHLSTLSE 376  
Db 169 EELRDLRLRAHVLAHQHVAQYSDLLRQMAARFEALKEGGGS-LAEYQAKAQQLKALGE 227  
QY 377 KAKPALEDLROGLLPVLESFVKVSLSALEEYTKKLTQ 414  
Db 228 KAKPALEDLROGLLPVLENLKVLSILAAIDEASKKLNAQ 265

RESULT 10  
A56858  
apolipoprotein A-I precursor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 05-Jan-1996 #sequence\_revision 23-Aug-1997 #text\_change 13-Aug-1999  
C:Accession: I45853; A56858; A34649  
R:O'Huigin, C.; Chan, L.; Li, W.  
Mol. Biol. Evol. 7, 327-339, 1990  
A:Title: Cloning and sequencing of bovine apolipoprotein A-I cDNA and molecular evolution  
A:Reference number: I45853; MUID:90348478; PMID:2117227  
A:Accession: I45853  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-265 <ORX>  
A:Cross-references: GB:M35870; NID:g162677; PIDN:AAA30381.1; PID:g162678  
R:Sparrow, D.A.; Lee, B.R.; Laplaud, P.M.; Aubeiron, S.; Bauchart, D.; Chapman, M.J.; G  
Biochim. Biophys. Acta 1223, 145-150, 1992  
A:Title: Plasma lipid transport in the perinatal calf, Bos spp: primary structure of h  
A:Reference number: A56858; MUID:92153895; PMID:1739745  
A:Accession: A56858  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 19-184, 'OL', 187-265 <SPA>  
A:Experimental source: Friesian-Holstein male calves aged 2-4 weeks  
A:Note: sequence extracted from NCBI backbone (NCBIP:83520)  
R:Aubeiron, S.; Sparrow, D.A.; Beaubatie, L.; Bauchart, D.; Sparrow, J.T.; Laplaud, P.M.  
Biochem. Biophys. Res. Commun. 166, 833-839, 1990  
A:Title: Characterization and amino-terminal sequence of apolipoprotein AI from plasma h  
A:Reference number: A34649; MUID:90147795; PMID:2105728  
A:Accession: A34649  
A:Molecule type: protein  
A:Residues: 25-70 <AUB>  
A:Experimental source: Friesian-Holstein male calves aged 2-4 weeks  
A:Superfamily: apolipoprotein A-I  
A:Keywords: lipid binding; lipoprotein  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-265/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 37.9%; Score 803; DB 2; Length 265;  
Best Local Similarity 58.6%; Pred. No. 8.6e-31;  
Matches 163; Conservative 29; Mismatches 42; Indels 44; Gaps 2;

QY 137 DELRQRLAARLEALKEKNGGARLAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFVK 196  
Db 32 DRVKDFATVYVDAIKSDGRDYVAQFEASALGHLN----- 60

QY 197 SFLSALEEYTKKLTQGTFLKLLDNWDSVTSTFSKLRQGLGVPVTOEFWDNLEKETEGLRQE 256  
Db 61 -----LGKQLNLKLLDNWDTLASTLSKVRQGLGVPVTOEFWDNLEKETASLRQE 108  
QY 257 MSKDLSEEVKAKVQPYLDLDFQKQWQEMELYRQKVEPLRAELQEGARQKHLQEKLSPLG 316  
Db 109 MHKDLSEEVKAKVQPYLDLDFQKQWQEMELYRQKVEPLRAELQEGARQKHLQEKLSPLA 168  
QY 317 EEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKEKNGGARLAEYHAKATEHLSTLSE 376

Db 169 QELDRARAHVETLRQHVAPYSDDLRLQRLTARLEALKEGGGS-LAEYHAKASEQLKALGE 227  
QY 377 KAKPALEDLROGLLPVLESFVKVSLSALEEYTKKLTQ 414  
Db 228 KAKPVLEDLROGLLPVLESKVSILAAIDEASKKLNAQ 265

RESULT 11  
S31394  
apolipoprotein A-I - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Aug-1999  
C:Accession: S31394  
R:Moehel, B.; Flach, R.; Weiss, B.; Weiler-Guettler, H.; Frey, A.; Zinke, H.; Gassen  
submitted to the EMBL Data Library, November 1992  
A:Description: Genomic organization of the porcine apolipoprotein A1 gene and study o  
A:Reference number: S31394  
A:Accession: S31394  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-264 <MOE>  
A:Cross-references: EMBL:X69477; NID:g1889; PIDN:CAA49234.1; PID:g1890  
C:Superfamily: apolipoprotein A-I

Query Match 37.6%; Score 796.5; DB 2; Length 264;  
Best Local Similarity 59.9%; Pred. No. 1.7e-30;  
Matches 167; Conservative 27; Mismatches 38; Indels 47; Gaps 4;

QY 137 DELRQRLAARLEALKEKNGGARLAEYHAKAT-EHLSTLSEKAKPALEDLROGLLPVLESFK 195  
Db 32 DRVKDFATVYVDAIKSDGRDYVAQFEASALGHLN----- 66

QY 196 VPSLSALEEYTKKLTQGTFLKLLDNWDSVTSTFSKLRQGLGVPVTOEFWDNLEKETEGLRQ 255  
Db 67 -----LKLNDWDSLGSTFTKVRQGLGVPVTOEFWDNLEKETALRQ 107

QY 256 ENSKDLSEEVKAKVQPYLDLDFQKQWQEMELYRQKVEPLRAELQEGARQKHLQEKLSPL 315  
Db 108 ENSKDLSEEVKAKVQPYLDLDFQKQWQEMELYRQKVEPLRAELQEGARQKHLQEKLSPL 166

QY 316 GEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKEKNGGARLAEYHAKATEHLSTLSE 375  
Db 167 AEELRDLRLRAHVLAHQHVAQYSDLLRQMAARFEALKE-GGDSLAEYQAKAQQLKALG 225

QY 376 EKAKPALEDLROGLLPVLESFVKVSLSALEEYTKKLTQ 414  
Db 226 EKAKPALEDLROGLLPVLENLKVLSILAAIDEASKKLNAQ 264

RESULT 12  
JQ0704  
apolipoprotein A-I - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 28-Oct-1994  
C:Accession: JQ0704  
R:Weiler-Guettler, H.; Sommerfeldt, M.; Papandrikopoulou, A.; Mischek, U.; Bonitz, D.  
J. Neurochem. 54, 444-450, 1990  
A:Title: Synthesis of apolipoprotein A-I in pig brain microvascular endothelial cells  
A:Reference number: JQ0704; MUID:90132667; PMID:2105375  
A:Accession: JQ0704  
A:Molecule type: mRNA  
A:Residues: 1-231 <WEI>  
A:Note: the authors translated the codon CAG for residue 124 as His and GAC for resid  
C:Superfamily: apolipoprotein A-I  
C:Keywords: cholesterol metabolism; HDL; lipid binding; lipid transport; lipoprotein;

Query Match 37.3%; Score 789.5; DB 2; Length 231;  
Best Local Similarity 61.3%; Pred. No. 3.1e-30;  
Matches 165; Conservative 26; Mismatches 31; Indels 47; Gaps 4;

QY 147 LEALKENGARLAHYHAKAT-EHLSTLSEKAKPALEDLROGLLPVLESFVKVSLSALEEY 205



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Db 9 VDAIKSGRDYVAQFEASALGKHLN----- 33
QY 206 TKKLTNTQGTLLKLLDNWDSVTSTFSKLRQGLGPVTOEFWDLNLEKTEGLRQEMSKDLEEVK 265
Db 34 -----LKLLDNWDSLGSTFTKVRQGLGPVTOEFWDLNLEKTEGLRQEMSKDLEEVK 84
QY 266 AKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHLEQKLSPLGQEMRDRARA 325
Db 85 KKQVQPYLDDFQKKWQEMELYRQKM-PLGAEPREGARQKVQELQKLSPLAELRLRLRA 143
QY 326 HYDALRTHLAPYSDELQRLAARLALKENGARLAAYHAKATEHLSYLSKAKPALEDL 385
Db 144 HVAALRQHVPYSDDLRQRMARFALKE-GGDSLAELYCAKAQEQKALGEKAKPALEDL 202
QY 386 RQGLLPVLESFKVSFLSALAEYTKKLTNQ 414
Db 203 RQGLLPVLENKVSIIAIDEASKKLNAQ 231

RESULT 13
S22420
apolipoprotein A-I precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C:Accession: S22420; S22421; A44364
R:Stoffel, W.; Mueller, R.; Binczek, E.; Hofmann, K.
Biol. Chem. Hoppe-Seyler 373, 187-193, 1992
A:Title: Mouse apolipoprotein AI, cDNA-derived primary structure, gene organisation and
A:Reference number: S22420; MUID:92281682; PMID:1596360
A:Accession: S22420
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-264 <STO>
A:Cross-references: EMBL:X64262; NID:950014; PIDN:CAA45560.1; PID:950015
A:Accession: S22421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <STR2>
A:Cross-references: EMBL:X64263; NID:950020; PIDN:CAA45561.1; PID:950021
R:Januzil, J.L.; Azrolan, N.; O'Connell, A.; Aalto-Setälä, K.; Breslow, J.L.
Genomics 14, 1081-1088, 1992
A:Title: Characterization of the mouse apolipoprotein ApoA-1/Apoc-3 gene locus: genomic.
A:Reference number: A44364; MUID:93122774; PMID:1478650
A:Accession: A44364
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-264 <JAN>
A:Note: sequence extracted from NCBI backbone (NCBIN:122400, NCBIPI:122407)
C:Genetics:
A:Introns: 15/1; 66/2
C:Superfamily: apolipoprotein A-I

Query Match 30.8%; Score 653; DB 2; Length 264;
Best Local Similarity 59.08; Pred. No. 7.3e-24;
Matches 128; Conservative 37; Mismatches 48; Indels 4; Gaps 2;

QY 198 FLSALEYTKKLTNTQGTLLKLLDNWDSVTSTFSKLRQGLGPVTOEFWDLNLEKTEGLRQEM 257
Db 52 YVSQFE--SSSLGQQLNLNLENDTLGTSVSQLQERLGLPLTRDFWDLNLEKETDWRQEM 109

QY 258 SKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHLEQKLSPLGE 317
Db 110 NKDLEEVKQKQVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHLEQKLSPLGE 317

QY 318 EMRDRARAHVDALRTHLAPYSDELQRLAARLALKENGARLAAYHAKATEHLSLSEK 377
Db 170 EFRDRMTHVDSLRTQLAPHSQEMRESLAQRLAELKSN--PTLNEYHTRAKTHLTKLGEK 227

QY 378 AKPALEDLRQGLLPVLESFKVSFLSALAEYTKKLTNQ 414
Db 228 ARPAALEDLRHSLMPLETLTKKAQSVIDKASSETITAQ 264
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RESULT 14
JC1237
apolipoprotein A-I precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-1993
C:Accession: JC1237
R:Boyle, T.P.; Marotti, K.R.
Gene 117, 243-247, 1992
A:Title: Structure of the murine gene encoding apolipoprotein A-I.
A:Reference number: JC1237; MUID:92347700; PMID:1639271
A:Accession: JC1237
A:Molecule type: DNA
A:Residues: 1-262 <BOY>
A:Cross-references: GB:M77801
C:Genetics:
A:Gene: ApoA-I
A:Introns: 15/1; 66/2
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport;
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-262/Product: apolipoprotein A-I #status predicted <MAT>

Query Match 30.5%; Score 647; DB 2; Length 262;
Best Local Similarity 61.1%; Pred. No. 1.4e-23;
Matches 127; Conservative 33; Mismatches 44; Indels 4; Gaps 2;

QY 198 FLSALEYTKKLTNTQGTLLKLLDNWDSVTSTFSKLRQGLGPVTOEFWDLNLEKTEGLRQEM 257
Db 52 YVSQFE--SSSLGQQLNLNLENDTLGTSVSQLQERLGLPLTRDFWDLNLEKETDWRQEM 109

QY 258 SKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHLEQKLSPLGE 317
Db 110 NKDLEEVKQKQVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHLEQKLSPLGE 317

QY 318 EMRDRARAHVDALRTHLAPYSDELQRLAARLALKENGARLAAYHAKATEHLSLSEK 377
Db 170 EFRDRMTHVDSLRTQLAPHSQEMRESLAQRLAELKSN--PTLNEYHTRAKTHLTKLGEK 227

QY 378 AKPALEDLRQGLLPVLESFKVSFLSALAE 405
Db 228 ARPAALEDLRHSLMPLETLTKKAQSVIE 255

RESULT 15
S21830
apolipoprotein A-I - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 20-Feb-1995 #sequence_revision 22-May-1998 #text_change 13-Aug-1999
C:Accession: S21830
R:Trievu, V.N.; Rohwer-Nuttler, P.; Black, D.D.
submitted to the EMBL Data Library, May 1991
A:Description: Sequence and developmental expression of porcine ApoA-I mRNA.
A:Reference number: S21830
A:Accession: S21830
A:Molecule type: mRNA
A:Residues: 1-164 <TRI>
A:Cross-references: EMBL:X59414; NID:g1891; PIDN:CAA42050.1; PID:g1892
A:Experimental source: liver
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid metabolism;

Query Match 29.2%; Score 617.5; DB 2; Length 164;
Best Local Similarity 76.5%; Pred. No. 1.9e-22;
Matches 124; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

QY 253 LRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHLEQKLSPLGE 312
Db 4 LRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHLEQKLSPLGE 312

QY 313 SPIGEMRDRARAHVDALRTHLAPYSDELQRLAARLALKENGARLAAYHAKATEHLS 372
Db 64 SPLAEELRSLRAHVQALRQHVAPYSDDLQRMARFALKEGGGS-LAEYQAKAQEQK 122
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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 30, 2003, 15:04:22 ; Search time 13 seconds  
(without alignments)  
1320.862 Million cell updates/sec

Title: US-09-990-087-17

Perfect score: 2118

Sequence: 1 MGHHHHHIEGRKLLDND.....SFKVSFLSALEYTKKLNQ 414

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1024	48.3	267	1 APAL_HUMAN	P02647 homo sapien
2	991.5	46.8	267	1 APAL_MACFA	P15568 macaca fasc
3	860.5	40.6	266	1 APAL_CANFA	P02648 canis famil
4	837	39.5	266	1 APAL_RABIT	P09809 oryctolagus
5	814	38.4	265	1 APAL_PIG	P18648 sus scrofa
6	798	37.7	265	1 APAL_BOVIN	P15497 bos taurus
7	701.5	33.1	265	1 APAL_TUPGS	Q18759 tupaia glis
8	653	30.8	264	1 APAL_MOUSE	Q00623 mus musculu
9	584	27.6	259	1 APAL_RAT	P04639 rattus norv
10	505.5	23.9	264	1 APAL_ANAPL	O42296 anas platyr
11	491.5	23.2	264	1 APAL_CHICK	P08250 gallus gall
12	470.5	22.2	264	1 APAL_COTUA	P32918 coturnix co
13	350.5	16.5	429	1 APAL_MACFA	P33621 macaca fasc
14	339.5	16.0	401	1 APAL_PAPAN	Q28758 papio anubi
15	320.5	15.1	396	1 APAL_HUMAN	P06727 homo sapien
16	316.5	14.9	382	1 APAL_PIG	O46409 sus scrofa
17	292.5	13.8	391	1 APAL_RAT	P02651 rattus norv
18	279	13.2	395	1 APAL_MOUSE	P06728 mus musculu
19	244	11.5	262	1 AP12_BRARE	O42363 brachydanio
20	238	11.2	262	1 AP12_ONCMY	O57524 oncorhynch
21	228.5	10.8	262	1 AP11_ONCMY	O57523 oncorhynch
22	224	10.6	262	1 APAL_SALTR	Q91488 salmo trutt
23	222.5	10.5	1102	1 MYSC_CHICK	P29616 gallus gall
24	222	10.5	1972	1 MYHB_MOUSE	O08638 mus musculu
25	214	10.1	879	1 RA50_SULTO	Q96958 sulfolobus
26	213	10.1	2230	1 GOGA_HUMAN	Q13439 homo sapien
27	210	9.9	1976	1 MYHA_BOVIN	Q27991 bos taurus
28	209.5	9.9	1978	1 MYHB_CHICK	P10587 gallus gall
29	209	9.9	1972	1 MYHB_HUMAN	P13549 homo sapien
30	208.5	9.8	1934	1 MYH7_MESAU	Q9uzc8 mesocricetu
31	208	9.8	880	1 RA50_PYRAB	O29230 archaeoglob
32	208	9.8	886	1 RA50_ARCFU	O29230 archaeoglob
33	208	9.8	978	1 RA50_AQUAE	O67124 aquifex aeo

34	207.5	9.8	1938	1 MYH4_RABIT	Q28641 oryctolagus
35	207	9.8	1972	1 MYHB_RABIT	P35748 oryctolagus
36	205.5	9.7	1935	1 MYH7_PIG	P79293 sus scrofa
37	205	9.7	1935	1 MYH7_HUMAN	P12883 homo sapien
38	205	9.7	1961	1 MYH9_RAT	O62812 rattus norv
39	204.5	9.7	1938	1 MYH9_AEQIR	P24733 aequipecten
40	204.5	9.7	1976	1 MYHA_HUMAN	P35580 homo sapien
41	203.5	9.6	1935	1 MYH7_RAT	P02564 rattus norv
42	203	9.6	986	1 GM13_RAT	O62839 rattus norv
43	203	9.6	1959	1 MYH9_CHICK	P14105 gallus gall
44	203	9.6	1976	1 MYHA_RAT	O9jlt0 rattus norv
45	202	9.5	281	1 APE_BRARE	O42364 brachydanio

## ALIGNMENTS

RESULT 1					
APAL_HUMAN					
ID	APAL_HUMAN	STANDARD;	PRT;	267 AA.	
DT	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Apolipoprotein A-I precursor (Apo-AI).				
GN	APOA1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84221405; PubMed=6328445;				
RA	Sharpe C.R., Sidoli A., Shelley C.S., Lucero M.A., Shoulders C.C.,				
RA	Baralle F.E.;				
RT	"Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA				
RT	abundance.";				
RL	Nucleic Acids Res. 12:3917-3932(1984).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=85026665; PubMed=6207999;				
RA	Seilhamer J.J., Protter A.A., Frossard P., Levy-Wilson B.;				
RT	"Isolation and DNA sequence of full-length cDNA and of the entire				
RT	gene for human apolipoprotein AI -- discovery of a new genetic				
RT	polymorphism in the apo AI gene.";				
RL	DNA 3:309-317(1984).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83220822; PubMed=6406984;				
RA	Shoulders C.C., Kornblitt A.R., Munro B.S., Baralle F.E.;				
RT	"Gene structure of human apolipoprotein AI.";				
RL	Nucleic Acids Res. 11:2827-2837(1983).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83220772; PubMed=6304641;				
RA	Cheung P., Chan L.;				
RT	"Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.";				
RL	Nucleic Acids Res. 11:3703-3715(1983).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84119464; PubMed=6198645;				
RA	Law S.W., Brewer H.B. Jr.;				
RT	"Nucleotide sequence and the encoded amino acids of human				
RT	apolipoprotein A-I mRNA.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 81:66-70(1984).				
RN	[6]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=86008382; PubMed=2995392;				
RA	Law S.W., Brewer H.B. Jr.;				
RT	"Tangier disease. The complete mRNA sequence encoding for				
RT	preproapo-A-I.";				
RL	J. Biol. Chem. 260:12810-12814(1985).				
RN	[7]				

RP SEQUENCE FROM N.A.  
RX MEDLINE=84016011; PubMed=6413973;  
RA Karathanasis S.K., Zannis V.I., Breslow J.L.;  
RT "Isolation and characterization of the human apolipoprotein A-I  
gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:6147-6151(1983).  
[8]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89377481; PubMed=2673706;  
RA Meglilevsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,  
RA Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,  
RA Holmquist L., Carlson L.A., Bollen A.;  
RT "Production of human recombinant proapolipoprotein A-I in Escherichia  
coli: purification and biochemical characterization.";  
RL DNA 8:429-436(1989).  
[9]  
RP SEQUENCE FROM N.A. (VARIANT TANGIER).  
RX MEDLINE=88196137; PubMed=3129297;  
RA Makrides S.C., Ruiz-Opazo N., Hayden M., Nussbaum A.L., Breslow J.L.,  
RA Zannis V.I.;  
RT "Sequence and expression of Tangier apoA-I gene.";  
RL Eur. J. Biochem. 173:465-471(1988).  
[10]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal muscle;  
RA Strausberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
[11]  
RP SEQUENCE OF 118-267 FROM N.A.  
RX MEDLINE=83091059; PubMed=6294659;  
RA Breslow J.L., Ross D., McPherson J., Williams H.W., Kurnit D.,  
RA Nussbaum A.L., Karathanasis S.K., Zannis V.I.;  
RT "Isolation and characterization of cDNA clones for human  
apolipoprotein A-I.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:6861-6865(1982).  
[12]  
RP SEQUENCE OF 19-27.  
RX MEDLINE=83256553; PubMed=6409108;  
RA Brewer H.B. Jr., Fairwell T., Kay L., Meng M., Ronan R., Law S.,  
RA Light J.A.;  
RT "Human plasma proapoA-I: isolation and amino-terminal sequence.";  
RL Biochem. Biophys. Res. Commun. 113:626-632(1983).  
[13]  
RP SEQUENCE OF 25-267.  
RX MEDLINE=78127331; PubMed=204308;  
RA Brewer H.B. Jr., Fairwell T., Larue A., Ronan R., Houser A.,  
RA Bronzert T.J.;  
RT "The amino acid sequence of human APOA-I, an apolipoprotein isolated  
from high density lipoproteins.";  
RL Biochem. Biophys. Res. Commun. 80:623-630(1978).  
[14]  
RP SEQUENCE OF 25-267.  
RX MEDLINE=75133493; PubMed=164450;  
RA Baker H.N., Gotto A.M. Jr., Jackson R.L.;  
RT "The primary structure of human plasma high density apolipoprotein  
glutamine I (ApoA-I). II. The amino acid sequence and alignment of  
cyanogen bromide fragments IV, III, and I.";  
RL J. Biol. Chem. 250:2725-2738(1975).  
[15]  
RP SEQUENCE OF 25-56.  
RX MEDLINE=88333387; PubMed=3047170;  
RA Yui Y., Aoyama T., Morishita H., Takahashi M., Takatsu Y., Kawai C.;  
RT "Serum prostacyclin stabilizing factor is identical to apolipoprotein  
A-I (Apo A-I). A novel function of Apo A-I.";  
RL J. Clin. Invest. 82:803-807(1988).  
[16]  
RP SEQUENCE OF 25-48.  
RX MEDLINE=89380318; PubMed=2506184;  
RA Manjunath P., Marcel Y.L., Uma J., Seidah N.G., Chretien M.,  
RA Chapdelaine A.;  
RT "Apolipoprotein A-I binds to a family of bovine seminal plasma  
proteins.";  
RL J. Biol. Chem. 264:16853-16857(1989).

RN [17]  
RX SEQUENCE OF 25-43.  
RX MEDLINE=88070603; PubMed=3120314;  
RA Prioli R.P., Ordoas J.M., Rosenberg I., Schaeffer E.J.,  
RA Pereira M.E.A.;  
RT "Similarity of cruzin, an inhibitor of Trypanosoma cruzi  
neuraminidase, to high-density lipoprotein.";  
RL Science 238:1417-1419(1987).  
[18]  
RP SEQUENCE OF 25-42.  
RC TISSUE=Heart;  
RX MEDLINE=95203287; PubMed=7895732;  
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;  
RT "The human myocardial two-dimensional gel protein database: update  
1994.";  
RL Electrophoresis 15:1459-1465(1994).  
[19]  
RP PALMITOYLATION.  
RX MEDLINE=86140194; PubMed=3005308;  
RA Hoeg J.M., Meng M.S., Ronan R., Fairwell T., Brewer H.B. Jr.;  
RT "Human apolipoprotein A-I. Post-translational modification by fatty  
acid acylation.";  
RL J. Biol. Chem. 261:3911-3914(1986).  
[20]  
RP PROCESSING.  
RX MEDLINE=83195100; PubMed=6405383;  
RA Zannis V.I., Karathanasis S.K., Keutmann H.T., Goldberger G.,  
RA Breslow J.L.;  
RT "Intracellular and extracellular processing of human apolipoprotein  
A-I: secreted apolipoprotein A-I isoprotein 2 is a propeptide.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:2574-2578(1983).  
[21]  
RP STRUCTURE BY NMR OF 190-209.  
RX MEDLINE=96270776; PubMed=8664326;  
RA Wang G., Treleaven W.D., Cushley R.J.;  
RT "Conformation of human serum apolipoprotein A-I(166-185) in the  
presence of sodium dodecyl sulfate or dodecylphosphocholine by 1H-NMR  
and CD. Evidence for specific peptide-SDS interactions.";  
RL Biochim. Biophys. Acta 1301:174-184(1996).  
[22]  
RP X-RAY CRYSTALLOGRAPHY (4.0 ANGSTROMS) OF 67-267.  
RX MEDLINE=98024124; PubMed=9356442;  
RA Borhani D.W., Rogers D.P., Engler J.A., Brouillette C.G.;  
RT "Crystal structure of truncated human apolipoprotein A-I suggests a  
lipid-bound conformation.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:12291-12296(1997).  
[23]  
RP VARIANT MILANO.  
RX MEDLINE=83109095; PubMed=6401735;  
RA Weisgraber K.H., Rall S.C. Jr., Bersot T.P., Mahley R.W.,  
RA Franceschini G., Sirtori C.R.;  
RT "Apolipoprotein A-Milano. Detection of normal A-I in affected  
subjects and evidence for a cysteine for arginine substitution in the  
variant A-I.";  
RL J. Biol. Chem. 258:2508-2513(1983).  
[24]  
RP VARIANT TANGIER.  
RX MEDLINE=83300108; PubMed=6412234;  
RA Schmitz G., Assmann G., Rall S.C. Jr., Mahley R.W.;  
RT "Tangier disease: defective recombination of a specific Tangier  
apolipoprotein A-I isoform (pro-apo A-I) with high density  
lipoproteins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:6081-6085(1983).  
[25]  
RP VARIANT NORWAY.  
RX MEDLINE=84289383; PubMed=6432779;  
RA Rall S.C. Jr., Weisgraber K.H., Mahley R.W., Ogawa Y., Fielding C.J.,  
RA Utermann G., Haas J., Steinmetz A., Menzel H.J., Assmann G.;  
RT "Abnormal lecithin:cholesterol acyltransferase activation by a human  
apolipoprotein A-I variant in which a single lysine residue is  
deleted.";  
RL J. Biol. Chem. 259:10063-10070(1984).  
[26]



## RESULT 3

APAL\_CANFA STANDARD; PRT; 266 AA.

AC P02646;

DT 21-JUL-1996 (Rel. 01, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Apolipoprotein A-I precursor (Apo-AI).

GN APOA1.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=90132271; PubMed=2515239;

RA Luo C.-C., Li W.-H., Chan L.;

RT "Structure and expression of dog apolipoprotein A-I, E, and C-I

RT mRNAs: implications for the evolution and functional constraints of

RT apolipoprotein structure.";

RT J. Lipid Res. 30:1735-1746(1989).

RN [2]

RP SEQUENCE OF 25-266.

RX MEDLINE=82142425; PubMed=6801039;

RA Chung H., Randolph A., Reardon I., Heiriksion R.L.;

RT "The covalent structure of apolipoprotein A-I from canine high

RT density lipoproteins.";

RT J. Biol. Chem. 257:2961-2967(1982).

RN [3]

RP SEQUENCE OF 25-57 AND 262-265.

RX MEDLINE=76210910; PubMed=179887;

RA Nakai T., Whayne T.F., Tang J.;

RT "The amino- and carboxyl-terminal sequences of canine apolipoprotein

RT A-I.";

RL FEBS Lett. 64:409-411(1976).

RN [4]

RP SEQUENCE OF 25-37.

RC TISSUE=Heart;

RX MEDLINE=98163340; PubMed=9504812;

RA Dunn M.J., Corbett J.M., Wheeler C.H.;

RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of

RT dog heart proteins.";

RL Electrophoresis 18:2795-2802(1997).

CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF

CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING

CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR

CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN

CC CHYLOMICRONS. SYNTHESIZED IN THE LIVER AND SMALL INTESTINE.

CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.

DR PIR: A03092; LPDGA1.

DR HSP: P02847; IAVI.

DR HSC-2DPAGE; P02648; DOG.

DR InterPro: IPR000074; Apolipoprotein.

DR Pfam: PF01442; Apolipoprotein; 1.

KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.

FT SIGNAL 1 18 BY SIMILARITY.

FT PROPEP 19 24 APOLOPOPROTEIN A-I.

FT CHAIN 25 266 10 X APPROXIMATE TANDEM REPEATS.

FT DOMAIN 67 266 1.

FT REPEAT 67 88 1.

FT REPEAT 89 110 2.

FT REPEAT 111 121 3 (HALF-LENGTH).

FT REPEAT 122 143 4.

FT REPEAT 144 165 5.

FT REPEAT 166 187 6.

FT REPEAT 188 209 7.

FT REPEAT 210 231 8.

FT REPEAT 232 242 9 (HALF-LENGTH).

FT REPEAT 243 266 10.

FT CONFLICT 168 168 A -> G (IN REF. 2).

FT CONFLICT 202 202 E -> Q (IN REF. 2).

FT CONFLICT 235 235 E -> Q (IN REF. 2).

FT CONFLICT 264 266 NAO -> A (IN REF. 3).

SQ SEQUENCE 266 AA; 30196 MW; A3202620C28A869D CRC64;

Query Match 40.6%; Score 860.5; DB 1; Length 266;

Best Local Similarity 62.9%; Pred. No. 1.2e-32;

Matches 175; Conservative 26; Mismatches 34; Indels 43; Gaps 1;

QY 137 DELRQRLAARLEALKENGARLAAYHAKATEHLSTSEKAKPALEDRLGGLLPVLESFV 196

DB 32 DRYKDLATVYVDKDSGRDYVAQFEASA----- 60

QY 197 SFLSALEEYTKLNTQGLTKLLDNWDSVTFSTFKLEQGLGPVTQEFWDNLEKETGLRQ 256

DB 61 -----LGKQINLKLLDNWDSLSVTYKLEQIGPVTQEFWDNLEKETGLRQ 108

QY 257 MSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHEQKLSPIG 316

DB 109 MSKDLEEVKQVQPYLDDFQKKWQEEVELYRQKVAPLGSELREGARQKLQELQKLSPLA 168

QY 317 EEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTSE 376

DB 169 EELDRARHVDALRAQLAPYSDDLRLAARLEALKEGGASLAAYHARASEQUSALGE 228

QY 377 KAKPALEDRLQGLLPVLESFVSKVLSALEEYTKKLTNQ 414

DB 229 KARPALEDRLQGLLPVLESFVSKVLSLAIDENYKLNQA 266

RESULT 4

APAL\_RABIT STANDARD; PRT; 266 AA.

AC P09809;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Apolipoprotein A-I precursor (Apo-AI).

GN APOA1.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=22AP AI; TISSUE=Small intestine;

RA Paraskevopoulou T.B., Kritis A., Zannis V.I.;

RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Intestine;

RX MEDLINE=88082866; PubMed=3121329;

RA Pan T.C., Hao O.L., Yamin T.T., Dai P.H., Chen B.S., Chen S.L.,

RA Kroon P.A., Chao Y.S.;

RT "Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit

RT apolipoprotein A-I is synthesized in the intestine but not in the

RT liver.";

RL Eur. J. Biochem. 170:99-104(1987).

RN [3]

RP SEQUENCE OF 25-266.

RX MEDLINE=87030294; PubMed=3095115;

RA Yang C., Yang T., Pownall H.J., Gotto A.M. Jr.;

RT "The primary structure of apolipoprotein A-I from rabbit high-density

RT lipoprotein.";

RL Eur. J. Biochem. 160:427-431(1986).

CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF

CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING

CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR

CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN

CC CHYLOMICRONS.







QY 137 DELRQRLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKV 196  
 Db 32 DRVKDFATVYVIAIKSDGRDYVAQFEASA----- 60  
 QY 197 SFLSALEYTKKLTQGTLLKLDNDVSTSTSKLREQLPVPTQEFWDNLEKETEGLRQE 256  
 Db 61 -----LGKQLNLKLDNDVTLASTLSKVRQGLPVTQEFWDNLEKETASLRQE 108  
 QY 257 MSKDLEEVKAKVQPYLDQFQKWOEMELYRQKVEPLRAELOEGAROKLHELQKLSPLG 316  
 Db 109 MHKDLEEVKQVQPYLDQFQKWOEMELYRQKVEPLRAELOEGAROKLHELQKLSPLA 168  
 QY 317 EEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAHYHAKATEHLSTLSE 376  
 Db 169 QELDRARAHVETLRQALAPYSDDLRLRLARLEALKEGGS-LAHYHAKASEQKALGE 227  
 QY 377 KAKPALEDLRQGLLPVLESFKVSFLSALEYTKKLTQ 414  
 Db 228 KAKPVEDLRQGLLPVLESFKVSFLSALEYTKKLTQ 265

## RESULT 7

APAL\_TUPGB STANDARD; PRT; 265 AA.  
 AC 018759;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Apolipoprotein A-I precursor (Apo-AI).  
 GN APOA1.  
 OS Tupiaia glis belangeri (Common tree shrew).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.  
 OX NCBI\_TaxID=9396;  
 RN [1]  
 RC TISSUE=Liver;  
 RA Lu X., Chen B., Zhao Y., Wang K., Xue H., Zeng W.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF  
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING  
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR  
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).  
 CC -!- SUBCELLULAR LOCATION: Extracellular.  
 CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN  
 CC CHYLOMICRONS (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.  
 CC  
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 CC send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF005638; AAB82326.1; -.  
 DR HSSP; P02647; IAV1.  
 DR InterPro; IPR000074; Apolipoprotein.  
 DR Pfam; PF01442; Apolipoprotein; 1.  
 KW plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 24  
 FT CHAIN 25 265  
 FT DOMAIN 67 265  
 FT REPEAT 67 88  
 FT REPEAT 89 110  
 FT REPEAT 111 121  
 FT REPEAT 122 143  
 FT REPEAT 144 165  
 FT REPEAT 166 187  
 FT REPEAT 188 209  
 FT REPEAT 210 231

FT REPEAT 232 242 9 (HALF-LENGTH).  
 FT REPEAT 243 265 10.  
 SQ SEQUENCE 265 AA; 30332 MW; 60076BC39FAEA165 CRC64;  
 Query Match 33.1%; Score 701.5; DB 1; Length 265;  
 Best Local Similarity 50.9%; Pred. No. 1.5e-25;  
 Matches 140; Conservative 41; Mismatches 51; Indels 43; Gaps 2;  
 QY 137 DELRQRLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKV 196  
 Db 32 DRVDRLANVYDAVKESG-----REVVSQLEASA----- 60  
 QY 197 SFLSALEYTKKLTQGTLLKLDNDVSTSTSKLREQLPVPTQEFWDNLEKETEGLRQE 256  
 Db 61 -----LGKQLNLKLDNDVTLGSTFKVHEHGLPVAQFEFKLEKETELRRE 108  
 QY 257 MSKDLEEVKAKVQPYLDQFQKWOEMELYRQKVEPLRAELOEGAROKLHELQKLSPLG 316  
 Db 109 INKLEDEVROKTFQFDEIQKQWEDLERYRQKVEPLSAQLREGAROKLHELQEVPTPLG 168  
 QY 317 EEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAHYHAKATEHLSTLSE 376  
 Db 169 EDLRSVRAVADTLRTOLAPYSEQMRKTLGARLEAIKEGGSASLAHYHAKASEQLSAIGE 228  
 QY 377 KAKPALEDLRQGLLPVLESFKVSFLSALEYTKKL 411  
 Db 229 KAKPVEDLRQGLMPWSEFKTVGLNVIDEAAKKL 263  
 RESULT 8  
 ID APAL\_MOUSE STANDARD; PRT; 264 AA.  
 AC Q00623;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apolipoprotein A-I precursor (Apo-AI).  
 GN APOA1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RX MEDLINE-92281682; PubMed-1596360;  
 RA Scofield W., Mueller R., Binczek E., Hofmann K.;  
 RT "Mouse apolipoprotein AI. cDNA-derived primary structure, gene  
 RT organisation and complete nucleotide sequence."  
 RL Biol. Chem. Hoppe-Seyler 373:187-193(1992).  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RX MEDLINE-93122774; PubMed-1478650;  
 RA Januzzi J.L., Azrolan N., O'Connell A., Aalto-Setälä K., Breslow J.L.;  
 RT "Characterization of the mouse apolipoprotein ApoA-1/Apoc-3 gene  
 RT locus: genomic, mRNA, and protein sequences with comparisons to other  
 RT species."  
 RL Genomics 14:1081-1088(1992).  
 RN [3]  
 RC SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF  
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING  
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR  
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).  
 CC -!- SUBCELLULAR LOCATION: Extracellular.  
 CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN  
 CC CHYLOMICRONS.  
 CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.  
 CC  
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-----  
 DR EMBL; X64262; CAA45560.1; -;  
 DR EMBL; X64263; CAA45561.1; -;  
 DR EMBL; L04149; -; NOT ANNOTATED\_CDS.  
 DR EMBL; L04151; -; NOT ANNOTATED\_CDS.  
 DR EMBL; BC019837; AAL19837.1; -;  
 DR PIR; S22420; S22420.  
 DR PIR; A44364; A44364.  
 DR HSSP; P02647; IAV1.  
 DR SWISS-2DPAGE; Q00623; MOUSE.  
 DR MGI; 88049; Apoal.  
 DR InterPro; IPR000074; Apolipoprotein.  
 DR Pfam; PF01442; Apolipoprotein; 1.  
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 24  
 FT CHAIN 25 264  
 FT DOMAIN 67 264  
 FT REPEAT 67 88  
 FT REPEAT 89 110  
 FT REPEAT 111 121  
 FT REPEAT 122 143  
 FT REPEAT 144 165  
 FT REPEAT 166 187  
 FT REPEAT 188 207  
 FT REPEAT 208 229  
 FT REPEAT 230 240  
 FT REPEAT 241 264  
 SQ SEQUENCE 264 AA; 30587 MW; C453FF2019634AAC CRC64;

Query Match 30.8%; Score 653; DB 1; Length 264;  
 Best Local Similarity 59.08%; Pred. No. 2.3e-23;  
 Matches 128; Conservative 37; Mismatches 48; Indels 4; Gaps 2;  
 QY 198 FLSSALEEYTKKINTQGTLLKLDNDWSDVTSFKLREQLGPVTOEFWDNLEKETEGLRQEM 257  
 Db 52 YVSQFE--SSSLGQQLNLLNLDNDWDTLGSVGRLEQLGPVTOEFWDNLEKETEGLRQEM 109  
 QY 258 SKDLEEVKAKVQPYLDDFQKWKQWQEMELYRQKVEPLRLEQLQEGARQKLHLEQKLSPLGE 317  
 Db 110 NKDLEEVKQKQPYLDDFQKWKQWQEMELYRQKVEPLRLEQLQEGARQKLHLEQKLSPLVAE 169  
 QY 318 EMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAHYHAKATEHLSTLSEK 377  
 Db 170 EFRDRMRTHVDSLRTQLAPHSQMSRESLAQRALAEKSN--PTLNHYHTRAKTHLTKLGK 227  
 Y 378 AKPALEDLRQGLLPVLESFKVSLSSALEEYTKKLTQ 414  
 Db 228 ARPALEDLRHSLMPLETLTKTKAQSVIDKASFTLTAQ 264

RESULT 9  
 ID APAL RAT STANDARD; PRT; 259 AA.  
 AC P04639;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Apolipoprotein A-I precursor (Apo-AI).  
 GN APOA1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 ON NCBI\_TaxID=10116;  
 RX MEDLINE=84207987; PubMed=6426956;  
 RA Poncin J.E., Martial J.A., Gielen J.E.;

RT "Cloning and structure analysis of the rat apolipoprotein A-I cDNA.";  
 RL Eur. J. Biochem. 140:493-498(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87008540; PubMed=3020028;  
 RA Haddad I.A., Ordovas J.M., Fitzpatrick T., Karathanasis S.K.;  
 RT "Linkage, evolution, and expression of the rat apolipoprotein A-I, C-  
 III, and A-IV genes.";  
 RL J. Biol. Chem. 261:13268-13277(1986).  
 RN [3]  
 RP SEQUENCE OF 1-45.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=82098162; PubMed=6798036;  
 RA Gordon J.I., Smith D.P., Alpers D.H., Schonfeld G.,  
 RA Strauss A.W.;  
 RT "The primary translation product of rat intestinal apolipoprotein A-I  
 mRNA is an unusual preprotein.";  
 RL J. Biol. Chem. 257:971-978(1982).  
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF  
 CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING  
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR  
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).  
 CC -1- SUBCELLULAR LOCATION: Extracellular.  
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN  
 CC CHYLOMICRONS.  
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.  
 CC -----  
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EMBL; M00001; AAA40749.1; -;  
 EMBL; X00538; CAA25224.1; -;  
 EMBL; J02597; AAA40745.1; -;  
 PIR; A24700; A24700.  
 DR HSSP; P02647; IAV1.  
 DR InterPro; IPR000074; Apolipoprotein.  
 DR Pfam; PF01442; Apolipoprotein; 1.  
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 24  
 FT CHAIN 25 259  
 FT DOMAIN 67 259  
 FT REPEAT 67 88  
 FT REPEAT 89 110  
 FT REPEAT 111 121  
 FT REPEAT 122 143  
 FT REPEAT 144 161  
 FT REPEAT 162 183  
 FT REPEAT 184 203  
 FT REPEAT 204 225  
 FT REPEAT 226 236  
 FT REPEAT 237 259  
 FT CONFLICT 201 201 R -> K (IN REF. 2).  
 FT CONFLICT 214 214 G -> S (IN REF. 2).  
 FT CONFLICT 218 218 R -> K (IN REF. 2).  
 SQ SEQUENCE 259 AA; 30088 MW; 2E8D5E845FEAE88 CRC64;

Query Match 27.6%; Score 584; DB 1; Length 259;  
 Best Local Similarity 54.9%; Pred. No. 2.7e-20;  
 Matches 118; Conservative 33; Mismatches 56; Indels 8; Gaps 3;  
 QY 198 FLSSALEEYTKKINTQGTLLKLDNDWSDVTSFKLREQLGPVTOEFWDNLEKETEGLRQEM 257  
 Db 52 YVSQFE--LGKQLNLLNLDNDWDTLGSVGRLEQLGPVTOEFWDNLEKETEGLRQEM 109  
 QY 258 SKDLEEVKAKVQPYLDDFQKWKQWQEMELYRQKVEPLRLEQLQEGARQKLHLEQKLSPLGE 317  
 Db 110 NKDLEEVKQKQPYLDDFQKWKQWQEMELYRQKVEPLRLEQLQEGARQKLHLEQKLSPLVAE 165

QY 318 EMRDRARHVDLRTHLAPYSDELRLORLAARLEAKENGARLAHEYHAKATEHLSTLSEK 377  
 DB 166 EFEDRMVNADALRAKFGIYSDQMRNLAQLRTIERNH--PTLIEYTKAGDHLRLTIGEK 223  
 QY 378 AKPALEDLRQGLLPVLESFVKSFLSALBEYTKKLN 412  
 DB 224 AKPALDDLQGLMPVLEAWKAKIMSWIDEAKKLN 258

RESULT 10  
 APAL ANAPL STANDARD; PRT; 264 AA.  
 AC O42296;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Apolipoprotein A-I precursor (Apo-AI).  
 GN APOA1.  
 OS Anas platyrhynchos (Domestic duck).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.  
 OX NCBI\_TaxID=8839;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Pekin breed; TISSUE=Liver;  
 RA Chen B., Lu X., Wang K., Xue H., Zeng W., Zhu D., Chi L.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF  
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING  
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR  
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).  
 CC -!- SUBCELLULAR LOCATION: Extracellular.  
 CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN  
 CC CHYLOMICRONS.  
 CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.  
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 CC -----  
 CC EMBL; U86131; AAB64381.1; .  
 DR HSP; P02647; IGW4.  
 DR InterPro: IPR000074; Apolipoprotein.  
 DR Pfam: PF01442; Apolipoprotein; 1.  
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.  
 FT SIGNAL 1 18 BY SIMILARITY.  
 FT PROPEP 19 24 BY SIMILARITY.  
 FT CHAIN 25 264 APOLOPOPROTEIN A-I.  
 FT DOMAIN 67 264 10 X APPROXIMATE TANDEM REPEATS.  
 FT REPEAT 67 88 1.  
 FT REPEAT 89 110 2.  
 FT REPEAT 111 121 3 (HALF-LENGTH).  
 FT REPEAT 122 143 4.  
 FT REPEAT 144 165 5.  
 FT REPEAT 166 187 6.  
 FT REPEAT 188 209 7.  
 FT REPEAT 210 231 8.  
 FT REPEAT 232 242 9 (HALF-LENGTH).  
 FT REPEAT 243 264 10.  
 SQ SEQUENCE 264 AA; 30659 MW; 7546F4BAF2846900 CRC64;

Query Match 23.9%; Score 505.5; DB 1; Length 264;  
 Best Local Similarity 43.9%; Pred. No. 9e-17;  
 Matches 104; Conservative 49; Mismatches 83; Indels 1; Gaps 1;

QY 174 EKAKPALEDLRQGLLPVLESFVKSFLSALBEY-TKKLNTQGLKLDNWDVSTFSLR 232  
 DB 25 DEFPALDRDLVDVYLETVKASGDKIAQAFSAVGKQLDLKLDNLDITGAAGAAKL 84

QY 233 EOLGPVTOEFDWNLKETEGLRQEMSKDLSEVKAKVOPVLDLDFQKWKQWEEMLYRQKVEP 292  
 DB 85 EDMAFYKREVMWLKDTESLRAELTKDLSEVKIRPFLDQFSKATKEELEYRQRLAP 144  
 QY 293 LRAELOEGRKHLHEKLSPLGSEMRDRARAHVDLRTHLAPYSDELRLORLAARLEAL 352  
 DB 145 VAEELKELTKOKVLMQOKLTPVAEARDRLRGHVEELRKNLAPYSDELRLKLSQKLEEI 204  
 QY 353 KENGARLAHEYHAKATEHLSTLSEKAPALEDLRQGLLPVLESFVKSFLSALBEYTK 409  
 DB 205 REKGIPQAAEYQAKVVEQLSNREKMTPLVDQFKERLTPYAENLKTFRISLLDELQK 261

RESULT 11  
 APAL CHICK STANDARD; PRT; 264 AA.  
 AC P08250;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Apolipoprotein A-I precursor (Apo-AI).  
 GN APOA1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88049703; PubMed=3118875;  
 RA Byrnes L., Luo C.-C., Li W.-H., Yang C.-Y., Chan L.;  
 RT "Chicken apolipoprotein A-I: cDNA sequence, tissue expression and  
 RL evolution."; Biochem. Biophys. Res. Commun. 148:485-492(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88152500; PubMed=3126099;  
 RA Ferrari S., Tarugi P., Drusiani E., Calandra S., Fregni M.;  
 RT "The complete sequence of chick apolipoprotein AI mRNA and its  
 expression in the developing chick."; Gene 60:39-46(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87222301; PubMed=3108248;  
 RA Rajavashisth T.B., Dawson P.A., Williams D.L., Shackelford J.E.,  
 RA Leberer H., Lusis A.J.;  
 RT "Structure, evolution, and regulation of chicken apolipoprotein A-I."; J. Biol. Chem. 262:7058-7065(1987).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92381402; PubMed=1512510;  
 RA Lamou-Fava S., Sastry R., Ferrari S., Rajavashisth T.B.,  
 RA Lusis A.J., Karathanasis S.K.;  
 RT "Evolutionary distinct mechanisms regulate apolipoprotein A-I gene  
 expression: differences between avian and mammalian apoA-I gene  
 transcription control regions."; J. Lipid Res. 33:831-842(1992).  
 RN [5]  
 RP SEQUENCE OF 25-44.  
 RX MEDLINE=83213468; PubMed=6406496;  
 RA Shackelford J.E., Leberer H.G.;  
 RT "Synthesis and secretion of apolipoprotein AI by chick breast  
 muscle."; J. Biol. Chem. 258:7175-7180(1983).  
 CC -!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF  
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING  
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR  
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).  
 CC -!- SUBCELLULAR LOCATION: Extracellular.  
 CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN  
 CC CHYLOMICRONS.  
 CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.



RESULT 13

ID	AP04_MACFA	STANDARD:	PRT:	429 AA.
DT	P33621;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	Apolipoprotein A-IV precursor (Apo-AIV).			
GN	AP04A.			
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
OC	Cercopithecinae; Macaca.			
OX	NCBI_TaxID=9541;			
ON	[1]			
NP	SEQUENCE FROM N. A.			
RC	TISSUE=Leukocyte;			
RC	MEDLINE=93129330; PubMed=8448212;			
RA	Osada J., Pocovi M., Nicolosi R.J., Schaefer E.J., Ordovas J.M.:			
RT	"Nucleotide sequences of the Macaca fascicularis apolipoprotein C-III			
RT	and A-IV genes."			
RL	Biochim. Biophys. Acta 1172:335-339(1993).			
CC	-1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND			
CC	CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN			
CC	LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR			
CC	COMPONENT OF HDL AND CHYLOMICRONS.			
CC	-1- SUBCELLULAR LOCATION: Extracellular.			
CC	-1- TISSUE SPECIFICITY: SECRETED IN PLASMA.			
CC	-1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH			
CC	22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-			
CC	MEMS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-			
CC	HELICAL, AND MANY OF THESE HELICES ARE PREDICTED TO BE HIGHLY ALPHA-			
CC	THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL			
CC	ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.			
CC	-1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; X68361; CAA48421.1; -			
DR	PIR; S29565; S29565.			
DR	PIR; S30195; S30195.			
DR	HSP; P02649; INFN.			
DR	InterPro: IPR000074; Apolipoprotein.			
DR	Pfam: PF01442; Apolipoprotein; 2.			
KW	Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal.			
FT	SIGNAL 1 20 BY SIMILARITY.			
FT	CHAIN 21 429			
FT	DOMAIN 33 330 13 X 22 AA APPROXIMATE TANDEM REPEATS.			
FT	REPEAT 33 330			
FT	REPEAT 33 54 1.			
FT	REPEAT 60 81 2.			
FT	REPEAT 82 103 3.			
FT	REPEAT 115 136 4.			
FT	REPEAT 137 158 5.			
FT	REPEAT 159 180 6.			
FT	REPEAT 181 202 7.			
FT	REPEAT 203 224 8.			
FT	REPEAT 225 246 9.			
FT	REPEAT 247 268 10.			
FT	REPEAT 269 286 11.			
FT	REPEAT 287 308 12.			
FT	REPEAT 309 330 13.			
FT	DOMAIN 372 420 GIU/GLN-RICH.			
FT	SEQUENCE 429 AA; 49876 MW; 3D458F551D0DB60C CRC64;			

Query Match 16.5%; Score 350.5; DB 1; Length 429;

### Query Match

Best Local Similarity 25.1%; Pred. No. 1.3e-09;  
Matches 100; Conservative 72; Mismatches 130; Indels 97; Gaps 10;

QY	17	DNWDSVSTFSKLREQLGPVTOEFWDNLEKETEGRLQEQMSKDLSEVKAKVOPYLDLDFQK	76
Db	64	DKLGEVNTYAGDLQKLVFPFATELHERLAKDSEKLEKEIRLEVEVRARLLPHANEVSQK	123
QY	77	WQEMELRYQKVEPLRAELQEGAROKLHELQEKLSPLGEEMRDRARAHVDALRTHLPAYS	136
Db	124	IGENVRELRQORLEPTDGLTQVNTQTQLRQLTTPYAQMREVLRENADSLQTSLRPHA	183
QY	137	DELRLRLAARLALKENGARLAEYHAKATEHLSTLSEKAPALDLRQGLLPVLESFKV	196
Db	184	DQLKAKIDONVEELKER-----LTPVADEFKV	210
QY	197	SFLSALAEYTKKLTQGTGLKLDNWDVSTFSKLREOLGPVTOEFWDNLEKETEGRLQE	256
Db	211	-----KIDQVEELRRSLAPYAQDAQEKLNHQLGLAFQ	244
QY	257	MSKDLSEVKAKVOPYLDLDFQKQWQEMELRYQKVEPLRAELQEGAROKLHELQEKLSPLG	316
Db	245	MKNNAEELKARLSAEBL-----RQLAPLAEDMRGNLRNTEGLOKSLAELG	293
QY	317	EEMRDRARAHVDALRTHLPAYSDELQRLAARLALKENGARLAEYHAKATE-HLSTLS	375
Db	294	GHL-DR--HVEEFLRVEPYGENFKALVQOMQLRKLGP-----HAGDVEGLHSFLE	344
QY	376	EKAKPALEDLROGLLPVLESFKV-SFLSALAEYTKKLTNT	413
Db	345	-----KDLRD-----KVNSFFSTFKESQDNT	367

RESULT 14

ID	AP44_PAPAN	STANDARD;	PRT;	401 AA.
AC	Q28756;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DE	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	Apolipoprotein A-IV precursor (Apo-AIV) (Fragment).			
GN	AP0A4.			
OS	Papio anubis (Olive baboon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Papio.			
ON	NCBI_TaxID=9555;			
RX	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Intestine;			
EX	MEDLINE=93340170; PubMed=8101842;			
RA	Hixson J.E., Kammerer C.M., Mott G.E., Britten M.L., Birnbaum S.,			
RA	Powers P.K., Vandeberg J.L.;			
RT	"Baboon apolipoprotein A-IV. Identification of Lys-76-->Glu that			
RT	distinguishes two common isoforms and detection of length			
RT	polymorphisms at the carboxyl terminus.;"			
RL	J. Biol. Chem. 268:15667-15673(1993).			
CC	-!- FUNCTION: MAY HAVE A ROLE IN CHLOMICRONS AND VLDL SECRETION AND			
CC	CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN			
CC	LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR			
CC	COMPONENT OF HDL AND CHYLOMICRONS.			
CC	-!- SUBCELLULAR LOCATION: Extracellular.			
CC	-!- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE INTESTINE.			
CC	-!- SECRETED IN PLASMA.			
CC	-!- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH			
CC	22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-			
CC	MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-			
CC	HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY			
CC	THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL			
CC	ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.			
CC	-!- POLYMORPHISM: THERE ARE TWO COMMON APOA-IV ISOFORMS, I (SHOWN			
CC	HERE) AND E. THE I ISOFORM IS ASSOCIATED WITH HIGHER LEVELS OF			
CC	HIGH DENSITY LIPOPROTEIN-C ON A HIGH CHOLESTEROL, SATURATED FAT			
CC	DIET.			

```
CC CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC CC -----
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CC CC -----
DR EMBL; L13174; AAA33379.1; -.
DR HSSP; P02649; INFN.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
DR Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal;
KW Polymorphism.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 401
FT DOMAIN 17 314
FT REPEAT 17 38
FT REPEAT 44 65
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FT REPEAT 99 120
FT REPEAT 121 142
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FT DOMAIN 356 394
FT VARIANT 80 80
FT SEQUENCE 401 AA; 46538 MW; 0A76D1284AA9837F CRC64;
Query Match 16.0%; Score 339.5; DB 1; Length 401;
Best Local Similarity 24.6%; Pred. No. 3.7e-09;
Matches 98; Conservative 73; Mismatches 131; Indels 97; Gaps 10;
QY 17 DNWDSVTSFKLRQLGPTQEFWDNLEKEETGLRQMSKDLVEVAKVQPYLDDQKK 76
DB 48 DKLGEVNTYAGDLQKKLVFFATHELHERLAKDSKKLKEIRKELEVEVRARLLPHANEVSQK 107
QY 77 WQEEMLYRQKVEPLRAELQEGARQKHELEKLSPLSEEMRDRARAHVDALRTHLAPYS 136
DB 108 IGVNRELOQRLEPYDQLRTQVNTQTQLRRLTPYAQMRLVRENADSLQTSLRPHA 167
QY 137 DELRQRLAARLEALKENGARLAHYAKATEHLSTLSEKAKPALEDLRLQGLLPVLESFKV 196
DB 168 DQKAKIDQNVBELGR-----LTPYADEFKV 194
QY 197 SFLSALEETKLNQGTGLKLDNWDVSTSFSLKRLQGLPVTOFFWBNLEKETEGLRQE 256
DB 195 -----KIDQVVEELRRSLAPYAQDAQKLNHLEGLAFQ 228
QY 257 MSKDLVEVAKVQPYLDDQKKWQEMELYRQKVEPLRAELOEGARQKHLBELQKLSPLG 316
DB 229 MKKNAELKARISAAEEL-----RQRLAPLAEDMRGNLRNTEGLQKSLAELG 277
QY 317 EEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAHYAKATE-HLSPLS 375
DB 278 GHL-DR---HVSEFRLRPEYGENFNKALVQOMEQLRKLGP-----HAGDVEGHLSPLE 328
QY 376 EKAKPALEDLRLQGLLPVLESFKV-SFLSALEETKLN 413
DB 329 -----KDLRD-----KVNSEFSTFKESQDNT 351
RESULT 15
APAA4_HUMAN STANDARD; PRT; 396 AA.
ID APAA4_HUMAN
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AC P06727;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apolipoprotein A-IV precursor (Apo-AIV).
GN APOA4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=89194198; PubMed=2930771;
RA Yang C., Gu Z.W., Xiong W., Rosseneu M., Yang H.X., Lee B.M.,
RA Gotto A.M. Jr., Chan L.;
RT "The primary structure of human apolipoprotein A-IV.";
RL Biochim. Biophys. Acta 1002:231-237(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87041474; PubMed=3095836;
RA Karathanasis S.K., Oettgen P., Haddad I.A., Antonarakis S.E.;
RT "Structure, evolution, and polymorphisms of the human apolipoprotein
RT A4 gene (APOA4).";
RL A gene (APOA4)."; Proc. Natl. Acad. Sci. U.S.A. 83:8457-8461(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86296629; PubMed=3755616;
RA Karathanasis S.K., Yunis I.;
RT "Structure evolution, and tissue-specific synthesis of human
RT apolipoprotein AIV.";
RL Biochemistry 25:3962-3970(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87250378; PubMed=3036793;
RA Elshourbagy N.A., Walker D.W., Paik Y.K., Boguski M.S., Freeman M.,
RA Gordon J.I., Taylor J.M.;
RT "Structure and expression of the human apolipoprotein A-IV gene.";
RL J. Biol. Chem. 262:7973-7981(1987).
RN [5]
RP SEQUENCE OF 21-396 FROM N.A.
RX MEDLINE=86111885; PubMed=3080432;
RA Elshourbagy N.A., Walker D.W., Boguski M.S., Gordon J.I., Taylor J.M.;
RT "The nucleotide and derived amino acid sequence of human
RT apolipoprotein A-IV mRNA and the close linkage of its gene to the
RT genes of apolipoproteins A-I and C-III.";
RL J. Biol. Chem. 261:1998-2002(1986).
RN [6]
RP SIGNAL SEQUENCE CLEAVAGE SITE.
RX MEDLINE=84161950; PubMed=6706947;
RA Gordon J.I., Bisgaier C.L., Sims H.F., Sachdev O.P., Glickman R.M.,
RA Strauss A.W.;
RT "Biosynthesis of human preapolipoprotein A-IV.";
RL J. Biol. Chem. 259:468-474(1984).
RN [7]
RP REVIEW ON POLYMORPHISM.
RA Lohse P., Brewer H.B. Jr.;
RT "Genetic polymorphism of apolipoprotein A-IV.";
RL Curr. Opin. Lipidol. 2:90-93(1991).
RN [8]
RP VARIANT A-IV*2.
RX MEDLINE=90277616; PubMed=2351649;
RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
RT "Genetic polymorphism of human plasma apolipoprotein A-IV is due to
RT nucleotide substitutions in the apolipoprotein A-IV gene.";
RL J. Biol. Chem. 265:10061-10064(1990).
RN [9]
RP VARIANTS A-IV*0 AND A-IV*3.
RX MEDLINE=90324273; PubMed=1973689;
RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
RT "Human plasma apolipoproteins A-IV*0 and A-IV*3. Molecular basis for
RT two rare variants of apolipoprotein A-IV-1.";
RL J. Biol. Chem. 265:12734-12739(1990).
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[illegible]

Search completed: April 30, 2003, 15:12:03  
Job time : 14 secs



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OM protein - protein search, using sw model

Run on: April 30, 2003, 15:09:57 ; Search time 87 Seconds  
(without alignments)  
980.500 Million cell updates/sec

Title: US-09-990-087-17  
Perfect score: 2118  
Sequence: 1 MGHHHHIEGRLLDNWD.....SFKYSFLSALEYTKLNTQ 414

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhmc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	741.5	35.0	264	11 Q922L4	Q922L4 mesocricetu
2	644.5	30.4	263	11 Q08855	Q08855 mus musculu
3	643.5	30.4	263	11 Q03042	Q03042 mus musculu
4	614	29.0	241	6 Q9TS49	Q9TS49 erinaceus e
5	582	27.5	258	11 Q09054	Q09054 rattus norv
6	580	27.4	258	11 Q08877	Q08877 rattus norv
7	340.5	16.1	366	13 Q93601	Q93601 gallus gall
8	327	15.4	67	4 Q9Y355	Q9Y355 homo sapien
9	283	13.4	435	11 Q01488	Q01488 mus musculu
10	275	13.0	395	11 Q91XF8	Q91XF8 mus musculu
11	272	12.8	395	11 Q9DBN0	Q9DBN0 mus musculu
12	251	11.9	1547	5 Q26471	Q26471 schistocerc
13	247	11.7	56	6 Q02762	Q02762 ovis aries
14	246	11.6	50	4 Q8TDB0	Q8TDB0 homo sapien
15	243.5	11.5	263	13 Q98TG6	Q98TG6 anguilla ja
16	233.5	11.0	244	4 Q13784	Q13784 homo sapien

17	225.5	10.6	1411	4	Q15075	Q15075 homo sapien
18	222	10.5	1935	5	Q44934	Q44934 loligo peal
19	222	10.5	1972	11	Q8R384	Q8R384 mus musculu
20	220	10.4	1344	5	Q9XVL5	Q9XVL5 schmidtea m
21	219.5	10.4	1410	4	Q14221	Q14221 homo sapien
22	219	10.3	1708	5	Q9U056	Q9U056 mytilus gal
23	218.5	10.3	1743	5	Q96063	Q96063 dugesia jap
24	217	10.2	1937	13	Q91BD4	Q91BD4 gallus gall
25	217	10.2	2310	5	Q9NKR1	Q9NKR1 leishmania
26	216.5	10.2	363	4	Q9UBJ3	Q9UBJ3 homo sapien
27	215.5	10.2	2354	5	Q9NKT9	Q9NKT9 leishmania
28	214	10.1	3187	11	Q63714	Q63714 rattus norv
29	212	10.0	623	4	Q9H2G3	Q9H2G3 homo sapien
30	211.5	10.0	1940	5	Q9U7E3	Q9U7E3 pecten maxi
31	211.5	10.0	2238	11	Q70365	Q70365 mus musculu
32	210.5	9.9	1390	4	Q8W2A3	Q8W2A3 mus sapien
33	210.5	9.9	1530	4	Q43241	Q43241 homo sapien
34	209.5	9.9	275	13	Q9FT02	Q9FT02 oncorhynch
35	209	9.9	1999	11	Q63731	Q63731 rattus norv
36	209	9.9	2138	5	Q9XZE3	Q9XZE3 amoeba prot
37	208	9.8	1931	13	Q42352	Q42352 cyprinus ca
38	206.5	9.7	1935	6	Q9BE39	Q9BE39 bos taurus
39	206.5	9.7	1935	11	Q91Z83	Q91Z83 mus musculu
40	206.5	9.7	1938	6	Q9BE40	Q9BE40 bos taurus
41	205.5	9.7	1498	4	Q8TDA9	Q8TDA9 homo sapien
42	205.5	9.7	1598	11	Q922D2	Q922D2 mus musculu
43	205.5	9.7	1935	6	Q9GKR1	Q9GKR1 sus scrofa
44	205.5	9.7	1939	6	Q9TV63	Q9TV63 sus scrofa
45	205.5	9.7	2007	13	Q02015	Q02015 gallus gall

ALIGNMENTS

RESULT 1

Q922L4	PRELIMINARY;	PRT;	264 AA.
ID	Q922L4;		
AC	Q922L4;		
DT	01-MAY-1999 (TrEMBLrel. 10, Created)		
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)		
DE	Apolipoprotein A-I.		
GN	APOAI.		
OS	Mesocricetus auratus (Golden hamster).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;		
OC	Mesocricetus.		
OX	NCBI_TaxID=10036;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=GOLDEN SYRIAN; TISSUE=INTESTINE;		
RX	MEDLINE=99061559; PubMed=9843713;		
RA	Wu J.Y.J., Reeves S.K., Wang Y.R., Wu Y., Lei P.P., Lei K.Y.;		
RT	"Zinc deficiency decreases plasma level and hepatic mRNA abundance of		
RT	apolipoprotein A-I in rats and hamsters.";		
RL	Am. J. Physiol. 275:CL516-CL525(1998).		
DR	EMBL; AF046919; AAC98484.1; -.		
DR	HSSP; P02647; IAV1.		
DR	InterPro; IPR000074; Apolipoprotein.		
DR	Pfam; PF01442; Apolipoprotein; 1.		
KW	Lipoprotein.		
SQ	SEQUENCE 264 AA; 30739 MW; 280B22F4C0F0B129 CRC64;		
Query Match 35.0%; Score 741.5; DB 11; Length 264;			
Best Local Similarity 63.5%; Pred. No. 5.3e-28;			
Matches 148; Conservative 30; Mismatches 44; Indels 11; Gaps 3;			
QY	191	LESEKVSFSALE----	TKKLTQGTLLKLDNWDVSTFSKLRQLQGPVTOE 241
Db	34	VKDFATVYDVADKDSGREGVTSQFETSA	LKLNLENLNDWTLGTVGRQLQGPVTOE 93
QY	242	FWDNLEKETGLRQEMSKDLEEVKAPVYLD	DFDKWQEEEMELYRQKVEPLRAELQSGA 301

RC	STRAIN=ICR AND BALB/C, AND C3H; TISSUE=SPLEEN;
RA	Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR	EMBL; U79575; AAB58427.1; -
DR	EMBL; U79572; AAB58424.1; -
DR	EMBL; U79573; AAB58425.1; -
DR	HSSP; P02647; IAV1.
DR	InterPro; IPR000074; Apolipoprotein.
DR	Pfam; PF01442; Apolipoprotein; 1.
KW	Lipoprotein.
SQ	SEQUENCE 263 AA; 30516 MW; E245DF7483A5A0DD CRC64;
Query Match 30.4%; Score 643.5; DB 11; Length 263;	
Best Local Similarity 59.0%; Pred. No. 2.1e-23;	
Matches 128; Conservative 37; Mismatches 47; Indels 5; Gaps 3;	
QY	198 FLSALEEYTKKLNQGTGLKLLDNWDSVTSFKLREQLPVTOEFWDNLEKETEGRLQEM 257
DB	52 YVSQFE--SSSLGQQLNLNLENDTLGSTVSQLQERLGLTRDFWDLNLEKETDQVROEM 109
QY	258 SKDLEEVKAKVQPYLDQFQKKWQEEVALYRQKVEPLRAELQEGARQKLHLEQELKSLPGE 317
DB	110 NKDLEEVKQVQPYLDQFQKKWKEDEVLYRQKVGPL-AELQESARQKLQELQGRLSVPAE 168
QY	318 EMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARGLAEYHAKATEHLSTLSEK 377
DB	169 EFRDRMTHVDSLRTQLAPHSEQMSRLAQLAELKSN--PTLNEYHTRAKTHLTKLGEK 226
QY	378 AKPALEDLROGLLPVLESFVKYSFSLSALEYTKKLNQ 414
DB	227 ARPALEDLRLHSLMPLETLTKRAQSVIDKASETLTAQ 263
RESULT 4	
ID	Q9TS49 PRELIMINARY; PRT; 241 AA.
AC	Q9TS49;
DT	01-MAY-2000 (Tremblrel. 13, Created)
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE	Apolipoprotein A-I, APOA-I-CHOLESTEROL transporter.
OS	Erinaceus europaeus (Western European hedgehog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
OX	NCBI_TaxID=9365;
RN	[1]
RP	SEQUENCE
RX	MEDLINE=95294458; PubMed=7775860;
RA	Sparrow D.A., Laplaud P.M., Saboureaux M., Zhou G., Dolphin P.J.,
RA	Gotto A.M.Jr., Sparrow J.T.;
RT	"Plasma lipid transport in the hedgehog: partial characterization of structure and function of apolipoprotein A-I.";
RL	J. Lipid Res. 36:485-495(1995).
DR	HSSP; P02647; IAV1.
DR	InterPro; IPR000074; Apolipoprotein.
DR	Pfam; PF01442; Apolipoprotein; 1.
SQ	SEQUENCE 241 AA; 27630 MW; 2EF00F2B69210535 CRC64;
Query Match 29.0%; Score 614; DB 6; Length 241;	
Best Local Similarity 53.3%; Pred. No. 4.5e-22;	
Matches 130; Conservative 35; Mismatches 73; Indels 6; Gaps 3;	
QY	174 EKAPAELEDLROGLLPVLESFVKYS---FLSALEYTKKLNQGTGLKLLDNWDSVTSFQK 230
DB	1 DEAKSYWDQIKDMLTVYDPTAKDSGKDYLTSLD--TSALGQQLNKKLADNNDTVSSALLK 58
QY	231 LREQLGPVTOEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDQFQKKWQEEVALYRQKV 290
DB	59 AREQMKPIAMEFQWGNLEKDTGLRQTVSKDLELVKEKQVQPYLDQFQKKWEELELYRQV 118
QY	291 EPLRAELQEGARQKLHLEQELKLSPLGEEEMDRARAHVDALRTHLAPYSDELQRLAARLE 350
DB	119 APLSAWEQARQAKAELOQKAGELGQQRDRVRTHVDALRTHLAPYSDELQRLAARLE 178

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QY 351 ALKENGARLAHVHAKATEHSTLSEKAPALDROGLLPVLESFKYSFSLALEYTKK 410
Db 179 DIKAKSG-DLAETQTKLSEHLKSFGEKAQPTLODLRHGLEPLWEGIKAGAMSLBELGKK 237
QY 411 LNTQ 414
Db 238 LNSQ 241

RESULT 5
ID O09054 PRELIMINARY; PRT; 258 AA.
AC O09054;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Apolipoprotein A-I.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WKI, AND SHRS; TISSUE-SPLEEN;
RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U79578; AAB58430.1; -
DR EMBL; U79577; AAB58429.1; -
DR HSSP; P02647; IAV1.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Lipoprotein.
SQ SEQUENCE 258 AA; 29918 MW; 093E6EF2E629CDC8 CRC64;

Query Match 27.5%; Score 582; DB 11; Length 258;
Best Local Similarity 54.4%; Pred. No. 1.5e-20;
Matches 117; Conservative 34; Mismatches 56; Indels 8; Gaps 3;

QY 198 FLSALEEYTKKLTQGTGLKLDNDVSTSTFSKLREQLGPGVTQDFWNLKETEGLRQEM 257
Db 51 YVSQESST--LGKQLNLNLDNDVSTGVRQLQEQLGPGVTQDFWANLEKETDWPFRNM 108
QY 258 SKDLEEVKAKVQPYLDQFKKQWQEMELYRQKVEPLRAELQEGARQKLHELQKLSPLGE 317
Db 109 NKDLNVKQKQPHLDFEQKWEVEAYRQKLEPLATELHKNAK----EMQRHLKVVAE 164
QY 318 EMRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAHYHAKATEHLSLSEK 377
Db 165 EFRDMRVNADALRAKFGLYSDQMRNLAQRLTEIKNH--PTLIEYHTKASDHLKTLGK 222
QY 378 AKPALEDLROGLLPVLESFKYSFSLALEYTKKLN 412
Db 223 AKPALDDLQGLMPVLEAWKAKIMSMIDEAKKKLN 257

RESULT 6
ID O08877 PRELIMINARY; PRT; 258 AA.
AC O08877;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Apolipoprotein A-I.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SHR; TISSUE-SPLEEN;
RX MEDLINE=98077648; PubMed=9415807;
RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;

Query Match 27.5%; Score 582; DB 11; Length 258;
Best Local Similarity 54.4%; Pred. No. 1.5e-20;
Matches 117; Conservative 34; Mismatches 56; Indels 8; Gaps 3;

QY 198 FLSALEEYTKKLTQGTGLKLDNDVSTSTFSKLREQLGPGVTQDFWNLKETEGLRQEM 257
Db 51 YVSQESST--LGKQLNLNLDNDVSTGVRQLQEQLGPGVTQDFWANLEKETDWPFRNM 108
QY 258 SKDLEEVKAKVQPYLDQFKKQWQEMELYRQKVEPLRAELQEGARQKLHELQKLSPLGE 317
Db 109 NKDLNVKQKQPHLDFEQKWEVEAYRQKLEPLATELHKNAK----EMQRHLKVVAE 164
QY 318 EMRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAHYHAKATEHLSLSEK 377
Db 165 EFRDMRVNADALRAKFGLYSDQMRNLAQRLTEIKNH--PTLIEYHTKASDHLKTLGK 222
QY 378 AKPALEDLROGLLPVLESFKYSFSLALEYTKKLN 412
Db 223 AKPALDDLQGLMPVLEAWKAKIMSMIDEAKKKLN 257

RESULT 7
ID O93601 PRELIMINARY; PRT; 366 AA.
AC O93601;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Apolipoprotein AIV.
GN APOAIV.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Callus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98221191; PubMed=9553114;
RA Steinmetz A., Hermann M., Nimpf J., Aebersold R., Ducret A.,
RA Weinberg R.B., Schneider W.J.;
RT "Expression and conservation of apolipoprotein AIV in an avian
species."
RL J. Biol. Chem. 273:10543-10549(1998).
DR EMBL; Y16534; CAA76273.1; -
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
KW Lipoprotein.
SQ SEQUENCE 366 AA; 40852 MW; B47DB49F3E8D91CE CRC64;

Query Match 16.1%; Score 340.5; DB 13; Length 366;
Best Local Similarity 23.2%; Pred. No. 4.7e-09;
Matches 91; Conservative 78; Mismatches 134; Indels 89; Gaps 6;

QY 15 LLDNDVSTSTFSKLREQLGPGVTQDFWNLKETEGLRQEMSKDLSEVKKVQPYLDQFQ 74
Db 61 LOSNQSANSYAEELQRRLPVPFATELQALQVODSQRLLKKQIQOELAELOAKLAPYDEVH 120
QY 75 KKWQEMELYRQKVEPLRAELQEGARQKLHELQKLSPLGEEMRDRARAHVDALRTHLAP 134
Db 121 QQIGTINIRELOAKLSPYADELRSQVDRGTGELRRALEFPATELREKLDQNSADSIQSLGP 180
QY 135 YSDELRLQRLAARLEALKENGARLAHYHAKATEHLSLSEKAKPALEDLROGLLPVLESF 194
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RT "Repetitive elements in the third intron of murine apolipoprotein A-I
RL gene.";
DR Biochem. Mol. Biol. Int. 43:989-996(1997).
DR EMBL; U79576; AAB58428.1; -
DR HSSP; P02647; IAV1.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Lipoprotein.
SQ SEQUENCE 258 AA; 29831 MW; 093FB582E629CDC8 CRC64;
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Query Match 27.4%; Score 580; DB 11; Length 258;
Best Local Similarity 54.4%; Pred. No. 1.9e-20;
Matches 117; Conservative 33; Mismatches 57; Indels 8; Gaps 3;

QY 198 FLSALEEYTKKLTQGTGLKLDNDVSTSTFSKLREQLGPGVTQDFWNLKETEGLRQEM 257
Db 51 YVSQESST--LGKQLNLNLDNDVSTGVRQLQEQLGPGVTQDFWANLEKETDWPFRNM 108
QY 258 SKDLEEVKAKVQPYLDQFKKQWQEMELYRQKVEPLRAELQEGARQKLHELQKLSPLGE 317
Db 109 NKDLNVKQKQPHLDFEQKWEVEAYRQKLEPLATELHKNAK----EMQRHLKVVAE 164
QY 318 EMRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAHYHAKATEHLSLSEK 377
Db 165 EFRDMRVNADALRAKFGLYSDQMRNLAQRLTEIKNH--PTLIEYHTKASDHLKTLGK 222
QY 378 AKPALEDLROGLLPVLESFKYSFSLALEYTKKLN 412
Db 223 AKPALDDLQGLMPVLEAWKAKIMSMIDEAKKKLN 257
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RESULT 7
ID O93601 PRELIMINARY; PRT; 366 AA.
AC O93601;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Apolipoprotein AIV.
GN APOAIV.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Callus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98221191; PubMed=9553114;
RA Steinmetz A., Hermann M., Nimpf J., Aebersold R., Ducret A.,
RA Weinberg R.B., Schneider W.J.;
RT "Expression and conservation of apolipoprotein AIV in an avian
species."
RL J. Biol. Chem. 273:10543-10549(1998).
DR EMBL; Y16534; CAA76273.1; -
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
KW Lipoprotein.
SQ SEQUENCE 366 AA; 40852 MW; B47DB49F3E8D91CE CRC64;
```

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Query Match 16.1%; Score 340.5; DB 13; Length 366;
Best Local Similarity 23.2%; Pred. No. 4.7e-09;
Matches 91; Conservative 78; Mismatches 134; Indels 89; Gaps 6;

QY 15 LLDNDVSTSTFSKLREQLGPGVTQDFWNLKETEGLRQEMSKDLSEVKKVQPYLDQFQ 74
Db 61 LOSNQSANSYAEELQRRLPVPFATELQALQVODSQRLLKKQIQOELAELOAKLAPYDEVH 120
QY 75 KKWQEMELYRQKVEPLRAELQEGARQKLHELQKLSPLGEEMRDRARAHVDALRTHLAP 134
Db 121 QQIGTINIRELOAKLSPYADELRSQVDRGTGELRRALEFPATELREKLDQNSADSIQSLGP 180
QY 135 YSDELRLQRLAARLEALKENGARLAHYHAKATEHLSLSEKAKPALEDLROGLLPVLESF 194
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Db 181 YAEKLOQIDSSVEGLK-----GQLTFLADELKEQVAQSVGLRKG----- 221
QY 195 KVSFLSALEYTKKLTNQGTGLKLDNWDVSTFSKLRQLGVPVTOFFWDLNLEKETEGLR 254
Db 222 -----LSPYAQEVQDGLNRQLQSLT 241
QY 255 QEMSKDLVEVKAKVQPYLDLDFQKKWOEEMELYRQKVEPLRAELQEGARQKLHELOEKLSP 314
Db 242 AQMERAAEELRSLAAS-----SEEM---RAQLSPLAQELQEAALRGDAEAMQORLAP 290
QY 315 LGEMDRARAHVDALRTHLAPYSDELQRRLAARLEALKENGARLAAYHAKATEHLSTL 374
Db 291 LAQQLDERLAQTVFAFPAQQAQISFETFRQQLVQRLEEMKQ-----KLESQTAGVEDHLDLL 346
QY 375 SEKAKPALEDLRQGLLPVLESFKVSFLSALEE 406
Db 347 KEVREKV-----ATFLSTTEQ 363

RESULT 8
QY355 PRELIMINARY; PRT; 67 AA.
AC QY355;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Apolipoprotein A1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA MEDLINE=99216322; PubMed=10198255;
RX Hamidi Asl K., Liepnieks J.J., Nakamura M., Parker F., Benson M.D.;
RT "A novel apolipoprotein A-1 variant, Arg173Pro, associated with
cardiac and cutaneous amyloidosis.";
RL Biochem. Biophys. Res. Commun. 257:584-588(1999).
DR EMBL; AF148963; AAD34604.1; -
DR HSP; P02647.1A1.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Lipoprotein.
FT NON_TER 1
FT NON_TER 67
FT NON_TER 67
SQ SEQUENCE 67 AA; 7433 MW; 5251FEB7BDD5AFB CRC64;

Query Match 15.4%; Score 327; DB 4; Length 67;
Best Local Similarity 98.5%; Pred. No. 3.2e-09;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

312 LSPGLGEEMDRARAHVDALRTHLAPYSDELQRRLAARLEALKENGARLAAYHAKATEHL 371
1 LSPGLGEEMDRARAHVDALRTHLAPYSDELQRRLAARLEALKENGARLAAYHAKATEHL 60

QY 372 STLSEKA 378
Db 61 STLSEKA 67

RESULT 9
Q01488 PRELIMINARY; PRT; 435 AA.
AC Q01488;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Variant apolipoprotein A-IV precursor (APOA-IV).
GN APOA-4.
OS Mus musculus castaneus (southeastern Asian house mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10091;

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RN SEQUENCE FROM N.A.
RP MEDLINE=91286309; PubMed=1648102;
RA Reue K., Leete T.H.;
RT "Genetic variation in mouse apolipoprotein A-IV due to insertion and
deletion in a region of tandem repeats.";
RL J. Biol. Chem. 266:12715-12721(1991).
CC !- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
LIPASE BY APOC-II: POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
COMPONENT OF HDL AND CHYLOMICRONS. IT MAY PLAY A ROLE IN THE
INTRAVASCULAR METABOLISM OF HDL. POTENTIAL ROLE IN CELLULAR
CHOLESTEROL EFFLUX.
CC !- TISSUE SPECIFICITY: INTESTINE, LIVER, AND PLASMA.
CC !- MISCELLANEOUS: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS
(EACH 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A & B, RELATED 11-
MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
HELICAL, & MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH
LECITHIN:CHOLESTEROL ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
CC !- MISCELLANEOUS: THE APOA-IV POLYMORPHISMS ARE CLASSIFIED BASED ON
THE OCCURENCE OF THREE, FOUR, OR FIVE E-Q-A-Q/ E-Q-Q-Q/ E-Q-V-Q
REPEAT UNITS.
CC EMBL; M64250; AAA37216.1; -
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
KW Lipid transport; HDL; VLDL; Chylomicron; Repeat; Signal; Liver;
KW Plasma; Multigene family; Polymorphism; Cholesterol metabolism.
FT SIGNAL 1 20
FT CHAIN 21 435
FT DOMAIN 374 393
FT REPEAT 374 377
FT REPEAT 378 381
FT REPEAT 378 381
FT REPEAT 382 385
FT REPEAT 386 389
FT REPEAT 390 393
FT REPEAT 435 AA; 49254 MW; B2AF55EEA8E456B2 CRC64;
SQ SEQUENCE 435 AA; 49254 MW; B2AF55EEA8E456B2 CRC64;

Query Match 13.4%; Score 283; DB 11; Length 435;
Best Local Similarity 22.7%; Pred. No. 2.8e-06;
Matches 83; Conservative 73; Mismatches 131; Indels 78; Gaps 7;

QY 24 STFSK-LRQLGVPVTOFFWDLNLEKETEGLRQEMSKDLVEVKAKVQPYLDLDFQKKWOEEME 82
Db 70 STYADGVRNKLVPFVVQVLSGHLAKETERVKEIKLEDLDRMMPHANKVVTQTGENMQ 129
QY 83 LYRQKVEPLRAELQEGARQKLHELOEKLSPGLGEEMDRARAHVDALRTHLAPYSDELQR 142
Db 130 KLOEHLKPYAVDLQDINTQTQEMKQLQTPYIORMQTTIKENVNLTSMPLATNLKDK 189
QY 143 LAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSAL 202
Db 190 FNRNMEELK-----GHLLTPRANELKATIDQN-----LEDLR----- 221
QY 203 EYTKKLINTQGLTKLDNWDVSTFSKLRQLGVPVTOFFWDLNLEKETEGLRQEMSKOLE 262
Db 222 -----SLAPITVGVQEKLNQHEGLAFQMKNAE 250
QY 263 EVKAKVQPYLDLDFQKKWOEEMELYRQKV-----EPLRAELQEGAR-----OKLHELOEKLSP 315
Db 251 ELQTKYSAKIDQLQKNLAPLVEDVQSKVNGTEGLQKSLKLDLNRQLEQQVVEEFRTVEPM 310
QY 316 GEEMDRARAHVDALRTHLAPYSDELQRRLAARLEALKENGARLAAYHAKATEHLSTLS 375
Db 311 GEMFNKALVQQLQFRQQLGPNSEGEVSHLSLFLEKSLRE-----KVNFSFMTLE 359
QY 376 EKAKP 380
Db 360 KKGP 364

RESULT 10
Q91XF8

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ID Q91XF8 PRELIMINARY; PRT; 395 AA.
AC Q91XF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Unknown (protein for MGC:18592).
GN APOA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010769; AAH10769.1; -.
DR MGD; MGI:88051; APOA4.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
SQ SEQUENCE 395 AA; 45029 MW; C48BE32EED441F71 CRC64;

Query Match 13.0%; Score 275; DB 11; Length 395;
Best Local Similarity 22.2%; Pred. No. 6e-06;
Matches 81; Conservative 74; Mismatches 132; Indels 78; Gaps 7;

QY 24 STFSK-LRQOLGPVTOEFWDNLEKETEGLRQEMSKDLREVKAKVQPYLLDDFOKKWOEME 82
DB 70 STYADGVHKNLVPFVQVLSGHLAQETERYKKEIKLELDQRDMPHANKVQTQFGENMQ 129
QY 83 LYRKVEPLRAELQEGARKHLEQKLSPLGEMDRARAHVDALRTHLAPYSDELQR 142
DB 130 KLQEHLPYAVDLDQINTQTEMKQLPTPIQRMQTTIKENVNLHTSMPLATNLKDK 189
QY 143 LAARLEALKENGARLAETHAKATEHLSTLSEKAKPALEDLRLQGLLPVLESFKVSFSL 202
DB 190 FNRNMEELK-----GHLTPRANELKATIDQN-----LEDLR----- 221
QY 203 EYTKKLNTQGTLLKLDNDVSTSTFSKLREQLGPVTOEFWDNLEKETEGLRQEMSKDL 262
DB 222 -----SLAPITVGQVQKLNHOMEGLAFOKKNAE 250
QY 263 EVKAKVQPYLLDDFOKKWOEMELYRKV-----EPLRAELQEGAR---QKLHLEQKLSPL 315
DB 251 ELQTKVSAKIDQLQKNLAPLVEDVQSVKNGTEGLQKSLDNLRLQEQVEEFRTVEPM 310
QY 316 GEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAETHAKATEHLSTLS 375
DB 311 GEMFNKALVQOLEQFRQOLGPNSEGEVSHLSFLEKSLRE-----KYNFSFMSTLE 359
QY 376 EKAKP 380
DB 360 KKGSP 364

RESULT 11
Q9DBNO PRELIMINARY; PRT; 395 AA.
AC Q9DBNO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Adult male liver cDNA, RIKEN full-length enriched library,
DE clone:1300002K10, full insert sequence.
GN APOA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LIVER;
RC MEDLINE=21085660; PubMed=11217851;

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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
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RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Togo-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK004856; BAB23620.1; -.
DR MGD; MGI:88051; APOA4.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
SQ SEQUENCE 395 AA; 45044 MW; 4102D84ACB0D182A CRC64;

Query Match 12.8%; Score 272; DB 11; Length 395;
Best Local Similarity 22.2%; Pred. No. 8.3e-06;
Matches 81; Conservative 73; Mismatches 133; Indels 78; Gaps 7;

QY 24 STFSK-LRQOLGPVTOEFWDNLEKETEGLRQEMSKDLREVKAKVQPYLLDDFOKKWOEME 82
DB 70 STYADGVHKNLVPFVQVLSGHLAQETERYKKEIKLELDQRDMPHANKVQTQFGENMQ 129
QY 83 LYRKVEPLRAELQEGARKHLEQKLSPLGEMDRARAHVDALRTHLAPYSDELQR 142
DB 130 KLQEHLPYAVDLDQINTQTEMKQLPTPIQRMQTTIKENVNLHTSMPLATNLKDK 189
QY 143 LAARLEALKENGARLAETHAKATEHLSTLSEKAKPALEDLRLQGLLPVLESFKVSFSL 202
DB 190 FNRNMEELK-----GHLTPRANELKATIDQN-----LEDLR----- 221
QY 203 EYTKKLNTQGTLLKLDNDVSTSTFSKLREQLGPVTOEFWDNLEKETEGLRQEMSKDL 262
DB 222 -----SLAPITVGQVQKLNHOMEGLAFOKKNAE 250
QY 263 EVKAKVQPYLLDDFOKKWOEMELYRKV-----EPLRAELQEGAR---QKLHLEQKLSPL 315
DB 251 ELQTKVSAKIDQLQKNLAPLVEDVQSVKNGTEGLQKSLDNLRLQEQVEEFRTVEPM 310
QY 316 GEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAETHAKATEHLSTLS 375
DB 311 GEMFNKALVQOLEQFRQOLGPNSEGEVSHLSFLEKSLRE-----KYNFSFMSTLE 359
QY 376 EKAKP 380
DB 360 KKGSP 364

RESULT 12
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AC Q26471;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE BLACKJACK protein.
OS Schistocerca americana (American grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Cyrtacanthacridinae;
OC Schistocerca.
OX NCBI_TaxID=7009;

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Search completed: April 30, 2003, 15:13:38  
Job time : 89 secs

